STIC-Biotech/ChemLib

From:

Swope, Sheridan

Sent:

Thursday, June 23, 2005 10:08 AM

To: Subject: STIC-Biotech/ChemLib RE: 10/617,433

10/617,443

10617443

Apologies!!

----Original Message----

From:

STIC-Biotech/ChemLib

Sent:

Thursday, June 23, 2005 6:33 AM

To: Subject:

Swope, Sheridan RE: 10/617,433

Good morning, do you have the correct number. 10/617433 is NO BIOTECH DATA.

----Original Message-----

From: Swope, Sheridan

Sent:

Wednesday, June 22, 2005 5:25 PM

STIC-Biotech/ChemLib

Subject: 10/617,433

For 10/617,433, pls search:

SID 1: residues 1-1038 oligo search (≥12 nts) against the NT databases.

SID 1: residues 1-1038 regular search against the NT databases.

SID 2: residues 1-9 against the NT databases.

SID 2: regular search against the NT databases.

Thanks!!!

Sheridan Swope, Ph.D. Patent Examiner, AU 1652 Recombinant Enzymes 571-272-0943 (voice) E02B71 Remsen Bld (Office) E02C70 Remsen Bld (Mailbox) Bonpo, Buten

STAFF USE ONLY Searcher: Searcher Phone: 2-Date Searcher Picked up: Date Completed: Searcher Prep/Rev. Time:

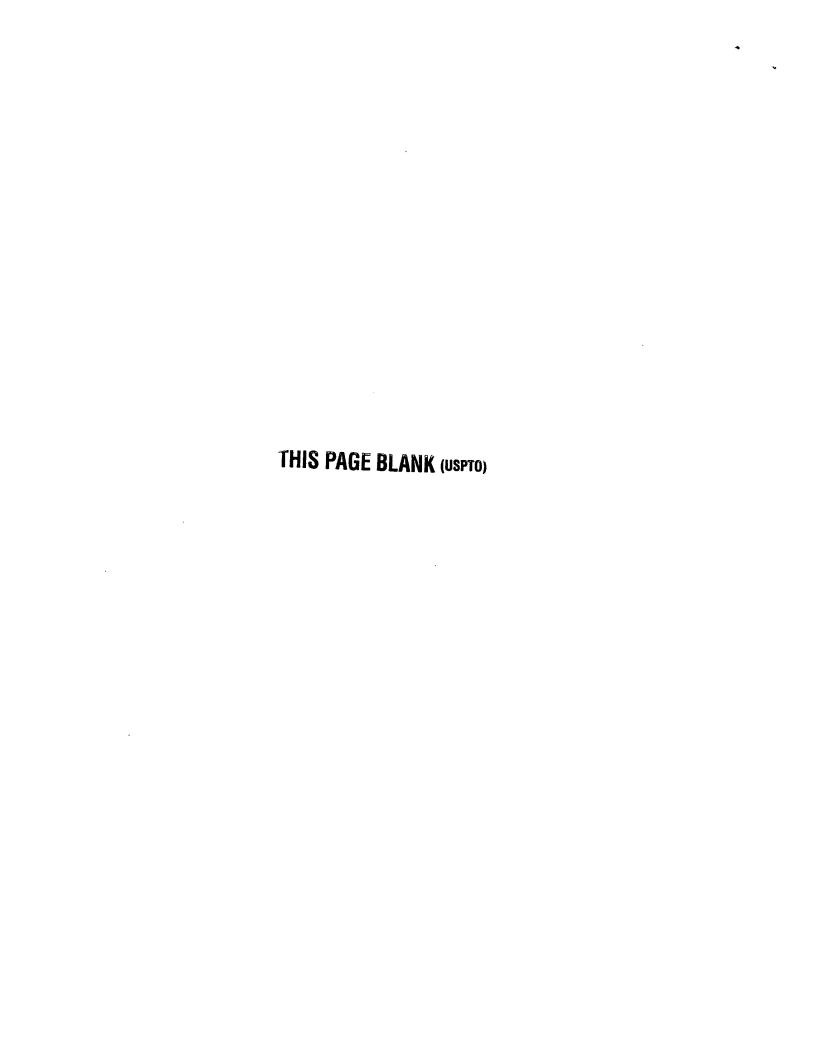
Online Time:_

Type of Search

NA#: AA#: Interference: SPDI: Oligomer: Encode/Transl: Structure#:_ Inventor:____ Litigation:_

Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM: WWW/Internet:_

Other(Specify):



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                          Database :
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Perfect score:
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1: gb_ba:*
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Gapop 10.0 , Gapext 1.0
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1038
1 cagggactcgaagtttgcag.....ggcccttcccgccagcgcag 1038
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10291.900 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	BB	ID	Description
!	-	1031.6	99.4	60597	إو	AC113611	1
	N	83	8.0	218856	N	AC122871	
a	w	77.2	7.4	235102	N	AC118993	
ი	4	77.2	7.4	258368	N	AC110369	
	v	77.2	7.4	264075	N	AC134075	•
	σ	56.4	5.4	125020	9	AF429315	
	7	56.2	5.4	172105	N	AC021197	
	œ	55.8	5.4	98501	9	AP005019	
ი	9	55.8	5.4	111282	6	AR368084	
ი 	10	55.8	5. 4.	111282	σ	AX662038	
	11	55.8	5.4	194719	N	AC026173	
	12	55.8	5.4	197022	N	AC055829	
α 	13	55.6	5.4	125020	9	AF429315	
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Ω 	16	53.2	5.1	192138	N	AC148545	
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4.7	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.9	٠,		4.9	4.9		·o	4.9	4.9				5.0		5.0	
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9	N	σ	2	N	9	9	9	φ	9	9	N	φ	N	N	N	N	9	9	ø	N	N	φ	9	9	N
AL355310	AC150795	AX655393	AC023920	AC020565	AP003780	AL590556	CNS01RH6	CNS05TC8	AL607038	AL390716	AC006184	AC002978	AC107358	AC106071	AC132705	AC147938	HSJ513G18	HSL118GA	AL161908	AC010936	AC089988	AC025033	AP000941	AP002954	AP000846
AL355310 Human DNA	AC150795 Bos tauru	AX655393 Sequence	Homo	AC020565 Homo sapi	AP003780 Homo sapi	AL590556 Human DNA	AL161662 Human chr	AL355074 Human chr	AL607038 Human DNA	Huma	AC006184 Homo sapi.	AC002978 Homo sapi	AC107358 Rattus no	AC106071 Rattus no	AC132705 Rattus no	AC147938 Ornithorh	AL109760 Human DNA	Z68881 Human DNA s	AL161908 Human DNA	AC010936 Homo sapi	AC089988 Homo sapi	AC025033 Homo sapi	AP000941 Homo sapi	AP002954 Homo sapi	AP000846 Homo sapi

ALIGNMENTS

REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	JOURNAL REFERENCE AUTHORS TITLE JOURNAL	AUTHORS TITLE JOURNAL MEDLINE MEDLINE PUBMED PUBMED REFERENCE AUTHORS	VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 AC113611 LOCUS DEFINITION
dicine, 4444 Forest Park Pa	MO 63108, USA 5 (bases 1 to 60597) 5 (bases 1. to 60597) Waterston,R.H. Direct Submission Submitted (23-FEB-2003) Genome Sequencing Center, Washington	63108, (bases terston rect sulpmitted liversit)	bequence of nome septeme services (2001) (bases 1 to 60597) (erston,R.H. rect Submission mitted (04-MAR-2002) Genome Sequencionstited (04-MAR-2002)	me se 8 (1:	AC113611.3 GI:28475761 AC113611.3 GI:28475761 HTG. HOmo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 60597)	AC113611 60597 bp DNA linear PRI 10-MAR-2003 Hdmo sapiens BAC clone RP11-421M20 from 4, complete sequence.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Data from AC104825 was used to finish this clone Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
This sequence is not the entire insert of the clone. This clone
overlapped by AC104650 and AC104825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Discrepant bases between AC104650, AC104825 and clone sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0421M20
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Best Local Similarity 99.6 Matches 1034; Conservative
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AGCTGGAGCCCATGAGGAGAGGGCCAGTTCTCTCTCTTAAGGGTATTGCTGTAGCATGAG
                                                                                                                                                                                                                                                                                   GGGGGTCTTCCACTACACCCCCGCCTGGACACTGCTGTAGCCCCCAGGGCTCGGAGGGACC
                                                                                                                                                                                                                                                                                                                                                    CTCTTTTGGCCCAGAGGGGCCACGCTGTGTCCGGGCCTGGGTAGCTCAGAAGGGTCACCT
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29613. .2
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27725. .28016
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Pred. No. 1.3e-201;
0; Mismatches 4;
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                                                                                     Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 217551 bases at least Q40
Consensus quality: 217980 bases at least Q20
Consensus quality: 218333 bases at least Q20
Insert size: 198000; agarose-fp
Insert size: 220194; sum-of-contigs
Quality coverage: 15.43 in Q20 bases; agarose-fp
Quality coverage: 13.45 in Q20 bases; sum-of-contigs
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Direct Submission
Submitted (28-MAY-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (08-AUG-2003) Genome Sequencing Center, 4444 For Parkway, St. Louis, MO 63108, USA
On Aug 8, 2003 this sequence version replaced gi:28461106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218856 bp Mus musculus chromosome UNK clone SEQUENCE, 5 unordered pieces. AC122871
                                                                                                                                                                                                                                                                                              Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                        Center project name: M_BA0107P12
                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson, R.K.
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McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of Mus musculus clone Unpublished
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 218856)
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AC122871.3 GI:33504638
HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson, R.K.
NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTTCCCGCCAGCGCAG 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Center ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome
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This record
                                                                                          GAATCTATAACCCAGCCAATGAGGAAGGGCCTCACGGAGGCC-AGCTGAGATGGCTCAGG 201444
                                                                                                                                                                                                                      TAGCAAGTCGGGCTGGGGGTGTGGCCAAGTTAGACACAGATGTAGGGCCCTGTGGACTCAG
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AGGGGCCCCAG 201455
                                                                                                                                                                                         TGGCAAGTAGGCCTGGGCTATGGCCAAGTTGGACAAAG--GCGGTGTTCTGTCCACTCAG
                                                                                                                                                                                                                                                                                 TTGCTGATGGCGGCAGAAATCTGAGCCAGTGATGAGGCTTTGGGGGCGTTCGTGCTGCC
                                                                                                                                                                                                                                                                                                                             CTGCTGACGGCAGCAGATCTGAGCCCGGGAAG-GGTCCAGGGAAGTTCGTGAACCATC
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                                              AGGGTCACCTG 541
                                                                                                                                        AAATTGGCAGCTCTTTTGGCCCAGAGGGGCCACGCTGTGTCCGGGCCTGGGTAGCTCAGA 530
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ilarity 60.1%;
Conservative
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121547. .218856
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/note="assembly_name:Contig15"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="UNK"
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1654: gap of unknown length
2784: contig of 1130 bp in length
2884: gap of unknown length
4846: contig of 1162 bp in length
4146: gap of unknown length
121446: contig of 117300 bp in length
121546: gap of unknown length
218856: contig of 97310 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    but the exact sizes of the gaps are unknown. d will be updated with the finished sequence it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GTGACCGAGACCGGGACCTGGAGGTCTC-----
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Pred. No. 1.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160; Indels 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 218856;
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                                                                                                                                                                                                                                                                                                 Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Alden, J., Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Allen, H., Albrocks, S., Amin, A., Anguiano, D., Allen, H., Albrocks, S., Alph, P., Brown, M., Barber, M., Barnstead, M., Benhmed, F., Bladdwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F., Biwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cher, C., Cho, J., Checko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Checko, J., Chavez, D., Chen, G., Chen, R., Cahder, M., Divya, K., Daval, B., Eaves, K., Bayah, M., Bacotto, M., Bugene, C., Bvans, C.A., Faller, F., Pan, G., Peraser, C.M., Gabis, A., Garcia, A., Garrer, T., Garza, M., Gebregovy, S., Rocer, K., Gill, R., Garcia, A., Garrer, T., Garza, M., Garra, W., Gunaratne, P., Haaland, M., Hamilton, C., Hamilton, K., Harrandez, S., Finley, M., Flagy, M., Forbee, L., Foster, M., Foster, P., Fraser, C.M., Gabis, A., Garra, M., Hernandez, R., Hines, S., Haldon, S. L., Hodgson, A., Hogues, M., Harrandez, R., Harrandez, R., Hines, S., Haldon, S. L., Hodgson, A., Hogues, M., Harrandez, R., Harrandez, R., Harrandez, R., Harrandez, R., Hull, S., Hully, S., Kully, S., Kan, Z., King, L., Kovar, C., Kwais, C., Hasia, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kcladd, H., Lozado, R.J., Liu, X., Ma, J., Liu, J., Liu,
                       Worley,K.C.
Direct Submission
Submitted (24-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235102)
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Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC118993 235102 bp DNA linear HTG 15-N
Rattus norvegicus clone CH230-237H8, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unordered pieces
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Genome Sequencing Consortium
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Best Local Similarity
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Li Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23681105.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/), Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
112 TCTGTCTGAGGCCACACAGCTAGAAAGCAGCCAGGCCCAGCCGAACCCCTGGTGTGTGCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a "working draft" sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                               GGGGTCCTCTTCAGTCCCACTTGTTAGATGGGAAAGTCAAGGCCCAGAGAGGGTAACAGA 89328
                                                                                                                        GAGGGCATATTCAGTCCCATTTTTCAGATGAG-GAGTTGAGGCCCCAGAGAACGTAAGTAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.990329
Consensus quality: 227037 bases at least Q40
Consensus quality: 229537 bases at least Q30
Consensus quality: 23525 bases at least Q20
Estimated insert size: 235071; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: CH230-237H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.b
Contact: hgsc-help@bcm.tmc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor Co
                                                                                                                                                                                    7.4%;
ilarity 58.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_end_extension
clone_end:Sp6"
complement(3003..3706)
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                        end_sequence:BZ101611"
108169. .110729
                                                                                                                                                                                                                                                                                                                                     /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:10116"
'clone="CH230-237H8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          one_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108068: contig of 108068 bp in length 108168: gap of unknown length 235102: contig of 126934 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _type="genomic DNA"
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ylor College of Medicine
                                                                                                                                                                                 Score 77.2; DB 2; Length 235102; Pred. No. 2.6e-06; 0; Mismatches 133; Indels 35;
                                                                                                                                                                                 Gaps
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	REFERENCE	RESULT 4 AC110369/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy Db 89	Qy Db 89	Оу ДЪ 89	Qу Дъ 89	Qy Db 89	68 qd
Gabisi, A., Ganta, R., Garcia, A., Garner, T., G. E., Geer, K., Gill, R., Grady, M., Guerra, W., G. Haaland, W., Hamil, C., Hamilton, C., Hamilton, Vlak, P., Hawes, A., Henderson, N., Hernandez, J. Hines, S., Hladun, S. L., Hodgson, A., Hogues, M. owells, S., Hulyk, S., Hume, J., Idlebird, D., J. acob, L., Jiang, H., Johnson, B., Johnson, R., J. ft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., ft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., ft, C. L., Lebow, H., Lozado, R. J., Lu, X., Ma, J., Mahindartne, M., Mahmoud, M., Malloy, K., Man pua, P., Martin, K., Martin, R., Martinez, E., Miner, G., Minja, E., Montemayor, J., Miner, G., Minja, E., Montemayor, J., A., Miner, G., Minja, E., Montemayor, J., Neal, D., Newton, N., Nguyen, N., Norris, S., Okwuonu, G., Olarnpuneagoon, A., Pal, S., Pa paul, H., Perez, A., Perez, L., Pfannkoch, C., pindexter, A., Popovic, D., Primus, E., Pu, LL.	Mammali, Butherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 258368) 1 (bases 1 to 258368) Muzny, D.Marie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Barbor, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davia, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Edgene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Edgene, C., Evans, C.A., Falls, T., Fan, G.,	AC110369 258368 bp DNA linear Rattus norvegicus clone CH230-49K10, *** SEQUENCING ***, 3 unordered pieces. AC110369 AC110369 AC110369 dG:23195246 HTG, HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED. Rattus norvegicus (Norway rat) Rattus norvegicus	409 TCTAGCAAGTCGGGCTGGGGTGTGGCCAAGTTAGACACAG 448	352 CTGCTGACGGCAGGAATCTGAGCCCGGGAAGGGTCCAGGGAAGTTCGTGAACCA 408	292 GCTGTAGGCCCCGTGCCACTGCATGCCTCAGGCCTGTGGTCCTGGCAGGCCACAGCCCTA 351	232 TGTTCCAGATGGTGGGAACTGGAGAGAGACCCCGGCACAGGCCCGTGCAGGGAACCCCCGAGG 291 9209 GTGGTGCCAGAACCCGGGACCTGGAAGGTCTCAGTACAGGCTCATGT	172 GCCCCCAGCCCAGTTGCTCATTGCGGGGGCTCGGGAGCCACGAGCGAG	

Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                  source
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On Sep 19, 2002 this sequence version replaced gi:21744398.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only be indicated in the feature table.
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Submitted (11-FEB-2002) Human Genome Sequencing Center, Department Submitted (11-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 258368)
Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: GRPY
Center clone name: CH230-49K10
Center clone name: CH230-49K10
Center clone name: CH230-49K10
Center clone name: CH230-49K10
Center clone name: Phrap; version 0.990329
Consensus quality: 236348 bases at least Q40
Consensus quality: 238877 bases at least Q20
Consensus quality: 240713 bases at least Q20
Estimated insert size: 259061; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                   102160
102260
249258
249358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                     Location,
                                             /mo1
                                                                            organism="Rattus norvegicus"
                                                                                                                      .258368
l_type="genomic DNA"
_xref="taxon:10116"
                                                                                                                                                                               102159: contig of 102159 bp in length 102259: gap of unknown length 249257: contig of 146998 bp in length 249357: gap of unknown length 258368: contig of 9011 bp in length.
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SOURCE
ORGANISM
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AC134075
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                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82321 GGGGTCCTCTTCAGTCCCACTTGTTAGATGGGAAAGTCAAGGCCCAGAGAGGGGTAACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 TCTGTCTGAGGCCACACAGCTAGAAAGCAGCCAGGCCCAGCCGAACCCCTGGTGTGCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 GAGGGCATATTCAGTCCCATTTTTCAGATGAG-GAGTTGAGGCCCCAGAGAACGTAAGTAA 111
1 (bases 1 to 264075)

Nuzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Albrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Bouck, J., Bwie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burch, J., Chavez, D., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC134075 bp 264075 bp 17 Rattus norvegicus clone CH230-2H18,
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_
                                                                                                                                                                                                                                                                                                                                                                                                                                  unordered pieces. AC134075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTAGCAAGTCGGGCTGGGGCCAAGTTAGACACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGTAGGCCCCGTGCCACTGCATGCCTCAGGCCTGTGGTCCTGGCAGCCCACAGCCCCTA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGTGCCAGAGACCGGGACCTGGAGGTCTCAGTACAGGCTCATGT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCTCAGTCCTGTACTCATTTTAGACTCCAGGGACCTCTCATAAGCACTGCCAAGCAGT 82144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTGACGGCAGGAATCTGAGCCCG---GGAAGGGTCCAGGGAAGTTCGTGAACCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTCCAGATGGTGGGAACTGGAGAGAGCCCGGCACAGGCCCGTGCAGGGAACCCCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----CACCCACATGCCTCAGGCCTGTGGTCCTGGCAAGCCACAGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="wgs_contig"
102260. .104120
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clone end:T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence:BH282841"
23...79518
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58.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 77.2; DB 2;
Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                      DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                    rat)
                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA linear HTG 13-NOV-2002 WORKING DRAFT SEQUENCE, 2
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Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hatr, M., Havlak, P., Hawes, A., Hernandez, J., Homes, C., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlson, E., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R., J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Lozado, R., J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Miner, G., Miner, G., Miner, G., Mickell, T., Mohabbat, K., Morgan, M., Nguyen, N., Nguyen, N., Nickerson, B., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, R., Payton, B., Perry, J., Perez, L., Peters, L., Pickenson, B., Payton, B., Pery, J., Perez, L., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Swatch, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Wang, S., Ward, Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Warren, R., Washington, C., Watlington, S., Walliamson, A., Warren, R., Washington, C., Watlington, S., Walliamson, A., Waeczyk, R., Wooden, S., Worley, K., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinston, R., Wang, S., Watlington, S., Walliamson, A., Waeczyk, R., Wooden, S., Watlington, S., Walliamson, A., Waeczyk, R., Wooden, S., Watlington, S., Walliamson, A., Walezzyk, R., Wooden, S., Watlington, S., Walliamson, A., Tamerisa, S., Walliamson, A., Walezzyk, R., Wooden, S., Watlington, S., Walliamson, A., Walezyk, R., Wooden, S., Walliamson, S., Walliamson, S., Walliamson, S., Walliamson, S., Wall
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On Nov 13, 2002 this sequence version replaced gi:23267440.
The sequence in this assembly is a combination of BAC based in the sequence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and the may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Barnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frar
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                                              Assembly program: Phrap; version 0.990329
Consensus quality: 228336 bases at least Q40
Consensus quality: 228408 bases at least Q30
Consensus quality: 238612 bases at least Q20
Estimated insert size: 229980; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: CH230-2H18
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NOTE: Estimated insert size may differ from sequence length
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Homo sap
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88538 CTTGTTACAGGGCACAGCTAAAAGAAAGCAGGTCCAGCTGGA--CCCAGTTGTGTGCA
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
TCTAGCAAGTCGGGCTGGGGTGTGGCCAAGTTAGACACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGTAGGCCCCGTGCCACTGCATGCCTCAGGCCTGTGGTCCTGGCAGCCACAGCCCCTA 351
                                                                                                                                                                                                                                                                                                                TGTTCCAGATGGTGGGAACTGGAGAGAGCCCGGCACAGGCCCGTGCAGGGAACCCCGAGG 291
                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGGCATATTCAGTCCCATTTTTCAGATGAG-GAGTTGAGGCCCCAGAGAACGTAAGTAA 111
                                                               TTGCTGATGGTGGCAGAAATCTGAGCCAGTGATGAAGGTTTTGGGGGGACGTTCATGTGCTG
                                                                                                              CTGCTGACGGCAGCAGGAATCTGAGCCCG---GGAAGGGTCCAGGGAAGTTCGTGAACCA 408
                                                                                                                                                                  -----CACCCACATGCCTCAGGCCTGTGGTCCTGGCAAGCCACAGCCCTG
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clone_end:Sp6"
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clone_end:T7"
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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clone_end:T7
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DNA gene,

linear partial cds

PRI 18-JAN-2002

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                                                                                                                                                        16955 WKWYSRGMSRSKSMRYTGGSKYMRSSMMCTSSCYASMCCMCCWSCCCMRSCCCMCRSYCC
                                          17075
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1 (bases 1 to 125020)

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hwang, H.S., Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice, A., Potter, N. T., Ross, C.A. and Margolls, R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 125020)
Holmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis, pirect Submission
                                                                                                                                                                                                                 MSMBMSVSYSVKMHSMHASBSCMHWBKCMTWSCCMSMMYKSSWWGSSWGMCCWGRRRSKG
                                                                                                                                                                                                                                             ACAGCTAGAAAGCAGCCAGGCCCAGCCGAACCCCTGGTGTGTGCAGCCCCAGCCCAGTT
                                                                                                                                                                                  GCTCATTGCGGGGGCTCGGGAGCCACGAGCGAGGCTGAGCATGTGTTCCAGATGGTGG
             GGAATCTGAGCCCGGGAAGGGTCCAGGGAAGTT--CGTGAACCATCTAGCAAGTCGGGCT
                                          KGGKSYGRKTKRKSRĠKMKGAKWYMYYRRSMRKMKMYSSKGMYCMYCWĊWĠRRĠCYCSĊM 17134
                                                                      CCACTGCATGCCTCAGGCCTGTGGTCCTGGCAGCCACAGCCCCTACTGCTGACGGCAGCA
                                                                                                   CMRYCCACKCYMSSYWTMSASYMSRRSYWKRSMKCWSRMCSRSRSSKCKSRGCGGSMGKG
                                                                                                                             GAACTGGAGAGAGCCCGGCACAGGCCCGTGCAGGGAACCCCGAGGGCTGTAGGCCCCGTG
                                                                                                                                                                                                                                                                           Conservative 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)" complement(35581..35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="synonym: JP3"
complement(<36507. .>36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="junctophilin 3"
complement (<36507. .36887)
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complement(<36507. .>36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_type=tandem
/rpt_unit="ctg"
                                                                                                                                                                                                                                                                                                                                                              /translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
4GFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="component of the junctional complex between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="JPH3"
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10.8%; Pred. No. 0.058;
tive 398; Mismatches 376;
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17315 WCMKMCYCMMRSWRSRGMSYYMYASWKSSSRGCYCTRCYWCMSSKSCYKSYYMMMRSKRM 17374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC021197
Homo mapiens chromosome 19 clone SEQUENCE, 21 unordered pieces.
                                                                                                                Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA On Jun 17, 2000 this sequence vareion washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCTTCCACTACA----CCCCCGCCTGGACACTGCTGTAGCCCCAGGGCTCGGAGGGACC 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTTCCCCCCNANTGGGGAAGCTTTTNCNKKTYSYYRKRNGCAMCKYNNYYNNSWRSSCR 17254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGTGTGGCCAAGTTAGACACAGATGTAGGGCCCCTGTGGACTCAGAAATTGGCAGCTCT
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 172105)
Waterston, R.H.
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AC021197.5
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                                     Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                          The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTÇACGGCAATATCCTAACCTÇTÇTÇTÇAGCCTGCCTGCCCAGCCTAGCAGGGTCCAGTG
Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGAMSCWRRCCYMRGASSMRAGSMSRRRAKGRSWGGRSKWWMIGGMWRSKYYYYCTGRRM 17614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : ::|::|: ::|::::::| | :::::|| | CWKRSGSMTSSCYYYSASSCMWMMSSKSCMCCCMMMKRRCACC 17777
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                                                                                   Genome Center ----
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RP11-798B19, WORKING DRAFT
                                                                    Sequencing
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                                                                                                                                                                            Louis,
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Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.99031 Consensus quality: 160434 bases at least 040 Consensus quality: 164353 bases at least 030 Consensus quality: 166763 bases at least 020 Consensus quality: 166763 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 185000; agarose-fp
Insert size: 170105; sum-of-contigs
Quality coverage: 3.66 in Q20 bases; agarose-fp
Quality coverage: 4.02 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; 100% Sequencing vector: plasmid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently
                    /clone="RP11-798B19"
i. .1301
                                               /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
note="assembly_name:Contigl1"
                                                                                                      6840y:
68509: gap of unknown recognitions of 8329 bp in length
76938: contig of 8329 bp in length
89902: contig of 11964 bp in length
89002: gap of unknown length
100235: contig of 11233 bp in length
110335: gap of unknown length
117760: contig of 17425 bp in length
117860: gap of unknown length
112316: contig of 24456 bp in length
142316: contig of 24456 bp in length
172105: contig of 29689 bp in length
172105: contig of 29689 bp in length
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             Homo sapiens (human)
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/note="assembly_name:Contigl3"
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142417. .172105
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17861. .142316
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52333. .59204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-MAR-2002) Masahira Hattori, The Institute of Physic and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa (B-mail: hattori@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/Tel:81-45-503-9111, Fax.81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA
Published Only in Database (2002)
2 (bases 1 to 99501)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Eujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                              1 (bases 1 to 111282)
Wei,M.-H., Wang,X., Merkulov,G.V., Di Francesco,V. and Beasley,E.N.
Isolated human phosphodiesterase proteins, nucleic acid molecules encoding human phosphodiesterase proteins, and uses thereof patent: US 6376225-A 3 23-APR-2002;
Location/Qualifiers
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Sequence 3 from patent US
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/clone="RP11-169D4"
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/chromosome="11"
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                                                     Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, O., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Liu, W., Liu, W., Liu, Y., Gong, L., Song, L., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, L., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, Y., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y.,
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Sequence 3 from Patent WO02053718.
AX662038
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Homo sapiens chromosome 3 clone RP11-169D4 map 3p,
IN PROGRESS ***, 62 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Chromosome 3p genomic sequence Unpublished
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of read
Assembly program: Phrap; version 0.990329
Consensus quality: 37507 bases at least Q40
Consensus quality: 45201 bases at least Q30
Consensus quality: 51060 bases at least Q20
Insert size: 52554; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen, J., Hu, S., Dong, W., Wang, J., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, O., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D., Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J. and Yang, H.
Direct Submission
Submitted (21-MAR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
                                                                                                                                                                                                                                                                                                                                                                               Quality coverage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-APR-2002) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Apr 5, 2002 this sequence version replaced gi:8101143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics, Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics, Chinese
100101, P.R.China
                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Interest bp in length
of 1235 bp in length
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itig of 1215 bp in length
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lg of 811 bp in length

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N. Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galgan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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                                                                                                                  Mammaira, William (Chases I to 197022)

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Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Birren, B., Chromosome 11, Clone RP11-796A3
                                                                                                         Homo sapiens chromosome 11, Unpublished
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                                                                                                                                                                                    Homo sapiens
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S., Severy, P., Royov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, Vo, A., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, N., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., Wu, X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., W.X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., W.X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., W.X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., W.X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., W.X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., W.X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., W.X., Wyman, D., Ye, W.J., Vo, A., Wisson, B., W.X., Wyman, D., Ye, W.J., Vo,
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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* arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence 
* as soon as it is available and the accession number wil
                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 193000; agarose-fp Insert size: 19302; sum-of-contigs Quality coverage: 4.5 in Q20 bases; agarose-fp Quality cov.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.960731 Consensus quality: 183643 bases at least Consensus quality: 189993 bases at least Consensus quality: 192582 bases at least consensus quality: 192582 bases at least
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Sequencing vector: M13; M77815; 96% of reads
Sequencing vector: Plasmid; n/a; %-0.f% of r
4.23053341508277Chemistry: Dye-terminator Big
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------ Project Information
Center project name: L8652
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11911. .13354
                                        /note="assembly_fragment"
13455. .15818
                                                                                        /note="assembly_fragment
                       /note="assembly_fragment"
                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
                                                                                                                                             /clone="RP11-796A3"
                                                                                                                              clone_lib="RPCI-11 Human
                                                                                                                                                         map="11"
                                                                                                                                                                                                         Jap of 100 bp

contig of 7453 bp 1...

gap of 100 bp

contig of 9198 bp in length

6 contig of 9276 bp in length

86 contig of 9276 bp in length

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125 gap of 100 bp

125 contig of 6439 bp in length

125 gap of 100 bp

1611 contig of 25036 bp in length

10261 gap of 100 bp

50677 contig of 10416 bp in length

150777 gap of 100 bp

163255 contig of 12478 bp in lengy

163255 contig of 22743 bp in lengy

186198 gap of 100 bp

186198 captig of 22743 bp in lengy

186198 captig of 100 bp

197022: contig of 10824 bp in lengy

1818 captig of 10824 bp in lengy
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g of 2879 bp :
f 100 bp
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Homo sapiens junctophilin 3 (JPH3)
AF429315
AF429315.1 GI:17646244
Holmes,S.B., Ingersorr-nounce
Direct Submission
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 125020)

Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
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                                                                                                                                                                                                                      Homo sapiens
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57486. .63567
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77691. .82259
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18538. .20675
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53668. .70096
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10197. .77590
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2175. .45912
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25516. .27880
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                                                  Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
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Location/Qualifiers
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/note="isolated from a patient
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complement(<36507. .>36887)
/gene="JPH3"
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/rpt_type=tandem
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/protein_id="AAL40941.1"
/protein_id="AAL40941.1"
/db_xref="G1:17646245"
/translation="MSSGGRENEDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
/translation="MSSGGRENEDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
HGFEVLGVYTWPSGUTVGGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
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/mol_type="genomic DNA"
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Street, Waltham, MA 02453,
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Genome Therapeutics Corporation Sequencing Center:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
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TITLE
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                                                                                                                                                                    Query Match
Best Local Similarity
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139619 GCCTGAAGCCACACAGCAGCCCAGAGGCCCACGCCC 139653
                                                                        115 GTCTGAGGCCACACAGCTAGAAAGCAGCCAGGCCC 149
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Homo sapiens chromosome 19 clone CTD-2562J15, complete sequence.
AC020911
AC020911.9 GI:29568021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-APR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Apr 5, 2003 this sequence version replaced gi:22128659. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 196512) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. .

1 (bases 1 to 196512)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                          Quality: Phrap Quality >=40 99.2% of Sequence; Estimated Total Number of Errors is 1.8. NOTE: 113bp single subclone 54713-54823.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
5 (bases 1 to 196512)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-AUG-2002) DOE Joint Genome Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inishing Completed at Stanford Human Genome Center
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OE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute.
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/note="NOTE: 113bp single subclone 54713-54823"
                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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72.6%;
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd

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SUMMARIES

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Ada03032 Human mCG	Abt10752 Human bre	Adm74471 Human car	Adc85355 Mouse Dpt	Adb72614 Human DPT	Ada02876 Human DPT	Abl98013 Human tes	Aal05121 Human rep		N	Aas32311 Human cDN	Ada71938 Rice gene	Aas32618 Human gen	Human	Aal03025 Human rep	Aba17415 Human ner	Aal03024 Human rep	Abs55190 Genomic D	Aal44261 Human pho	Adj11355 Human PRS	Description .	

New isolated S2 serine protease nucleic acids and polypeptides, useful for diagnosing and/or treating diseases with aberrant expression or activity the S2 serine protease, such as osteoarthritis, stress and apoptotic disorders.

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Human	Adj54477 Human B7-	Acn44566 Human gen	Adl13866 Osteoarth	Aah09370 Human cDN	Abq77243 Human MAR	Aba19604 Human ner	Aak87020 Human imm	Aba19605 Human ner	Aak87021 Human imm	Aah17445 Human cDN	Continuation (6 of	Continuation (4 of	Adf51132 Human P-R	Acn44158 Human gen	Adb62282 Human cDN	Aac87363 Human dev	Adq97289 Human can	Abl98014 Human tes	Aal05122 Human rep	Acn45182 Human gen	Aak67071 Human imm	Adm74627 Human car	Adc85512 Human gen	

ALIGNMENTS

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RESULT 1
ADJ11355
human; PRSS11-L; gene; ss; S2 serine protease; S2/HtrA; cellular physiology; apoptosis; gene therapy; osteoarth apoptotic; osteopathic; antiarthritic; tranquiliser.
                                            WPI; 2004-081723/08.
P-PSDB; ADJ11356.
                                                                        Darrow AL, Ql J, Chen C,
                                                                                                                                       03-JUL-2002; 2002US-00189099
                                                                                                                                                         03-JUL-2002; 2002US-00189099
                                                                                                                                                                            08-JAN-2004.
                                                                                                                                                                                               US2004005659-A1.
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                     Human PRSS11-L cDNA encoding a serine protease SeqID 1.
                                                                                                                                                                                                                                                                                                                                        20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                           ADJ11355;
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                                                                                        (DARR/) DARROW A L.
(QLJJ/) QL J.
(CHEN/) CHEN C.
(ANDR/) ANDRADE-GORDON P.
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                 /product= "PRSS11-L protein"
                                                                        Andrade-Gordon P;
                                                                                                                                                                                                                                                                                                                                                                             ВP
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Matches 1038
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                                       GCTCACGGCAATATCCTAACCTCTCTCTGAGCCTCCTGCCCAGCCTAGCAGGGTCCAGTG
                                                                                                                                                                                           GGAACAGACAAGGCCCAGGGGGACTAACCCGAGATCCAGCCCCGGCCTCACTCCCGTGTG
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GCTCACGGCAATATCCTAACCTCTCTCTGAGCCTCCTGCCCAGCCTAGCAGGGTCCAGTG
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/*tag= k /standard_name= replace(6133, G)	/standard_name= replace(6060, C)	e (/ 553 /standard_name= replace(5649, G) /*tag= i	/*tag= y /standard_name= replace(4734, A) /*tag= h	/standard_name= replace(4661, T)	/standard_name= replace(3710, G)	/standard_name= replace(3702, A)	/standard_name= replace(2986, A)	/standard_name= replace(2653, A)	/standard_name= replace(1997, T)	Location/Qualifi replace(254, A) /*tag= a		ne therapy rotein; PD pulmonary	esterase protein	irst entry)		DNA; 111282 B	CCTTCCCGCCAGCGCAG 1038	cceccaececae 1038	CTGGGCATAGGCCTCTG	CTGGGCATAGGCCTCTG	GGCTGAGGCTGGCTCTG	GGCTGAGGCTGGCTCTG	CCAAATGCCTGGTGTCA	ない なる かかのののかのでからない (本の)	GTGAGGAAGCCCAGCAC
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14-AUG-2000;
14-AUG-2000;
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2000US-0217496P.
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2000US-0255274P.
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2000US-0214886P.
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17-JAN-2001;
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                                                                                                                                                                                              reproductive system
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89; Conserv
                                                                                                                                                                                  gene therapy;
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2000US-0190076P
2000US-0198123P
                                             2000US-0180628P
2000US-0184664P
                                                                    2000US-0179065P
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replace(31224,C)
/*tag= bi
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17-NOV-2000;
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06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                 used
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 ABA17415;
                                                                                                                                                                                                                                                                       Sequence 7086
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 5712; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding a reproductive system antigen used in preventing, treating or ameliorating a medical condition.
                            ABA17415 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-)
                                                                                                   4383
                                                                                                                                                       4323 CTCATTTTATAGATGAAACACTGGGGCCTAGAGATAAGTAATCTCTCCAAGGCCACA 4382
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                                                                                                                    CAGCTAGAAAGCAGCCAGGCCCAGCCGAACCCCTGGTGTGTG 169
                                                                                                                                                                           CAGCTAGGAAGTAGCAGAGCTTATGCCACGTCAGGGTTTGTG
                                                                                                                                                                                                              5.0%;
milarity 69.6%;
Conservative
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2000US-0251989P
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                             DNA; 7086 BP
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                                                                                                                                                                                                                 0;
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pred. No. 0.0036;
0; Mismatches 31;
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14-AUG-2000
18-AUG-2000
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23-AUG-2000
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01-SEP-2000
01-SEP-2000
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18-APR-2000
19-MAY-2000
07-JUN-2000
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07-JUL-2000
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11-AUG-2000
14-AUG-2000
15-SEP-2000
01-SEP-2000
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
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02-OCT-2000;
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13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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2000US-024
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2000US-0246611P
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RESULT 6
AALOJOE
ID AALO
XX AALO
XX AALO
XX AALO
XX Z1-N
DT 21-N
XX XX
DE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel genes (ABA1104-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing CC; (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) CC infectious diseases such as viral, bacterial, fungal and parasitic CC infectious. Note: The sequence data for this patent did not form part of CC the printed specification, but was obtained in electronic format directly CC from WIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches 71
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11-DEC-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; {\tt ds}.
                                                                                                                                                                                                                      AAL03025 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding useful for preventing,
                                                                                                                  Human reproductive system related antigen DNA SEQ ID NO: 5713.
                                                                                                                                                     21-NOV-2001
                                                                                                                                                                                    AAL03025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7086 BP; 1264 A; 2050 C; 1979 G; 1793 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 9746; 1701pp + Sequence Listing; English.
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                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                       CAGCTAGGAAGTAGCAGAGCTTATGCCACGTCAGGGTTTGTG 4424
                                                                                                                                                                                                                                                                                                                                     CAGCTAGAAAGCAGCCAGGCCCAGCCGAACCCCTGGTGTGTG 169
                                                                                                                                                                                                                                                                                                                                                                        CTCATTTTATAGATGAAACACTGGGGCCTAGAGAAAGATAAGTAATCTCTCCAAGGCCACA
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diagnosing
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Pred. No. 0.00:
0; Mismatches
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24-FEB-2000;
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13-OCT-2000;
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                   Rosen
                                                   (HUMA-) HUMAN
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2000US-0251988P.
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2000US-024994P.
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2000US-0251990P
2000US-0254097P
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               SC,
                 Ruben
               MS.
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                                                                                       Matches
                                                                                                 Query Match
Best Local
                                                                                                                                                number of human reproductive system related antigens. These can keep the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encorprotein of the invention
                                                                                                                                                                                                                                            Isolated
used in p
                                                                                                                                 Sequence 7388
                                                                                                                                                                                                                        Disclosure;
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  4387
                                            4327
                      128
                                                                 68
                                                                                                 Similarity
                                                                                                                                                                                                                                            inucleic acid molecule encoding a reproductive system and preventing, treating or ameliorating a medical condition
CAGCTAGGAAGTAGCAGAGCTTATGCCACGTCAGGGTTTGTG
                     CAGCTAGAAAGCAGCCAGGCCCAGCCGAACCCCTGGTGTGTG 169
                                            CTCATTTTATAGATGAAACACTGGGGCCTAGAGAAGATAAGTAATCTCTCCAAGGCCACA 4386
                                                               Conservative
                                                                                                                                                                                                                        SEQ ID NO
                                                                                                                                 BP; 1347 A;
                                                                                                5.0%;
                                                                                                                                                                                                                       5713; 1297pp +
                                                                                                                                 2127 C;
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                                                                                                 Score 52.4;
Pred. No. 0.
                                                                                       Mismatches
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Human nervous system related polynucleotide ABA17416 ABA17416 23-JAN-2002 standard; DNA; 7388 (first entry) BP. SEQ ID ö

Human; nootropic; neuroprotective; cytostatic; dermatological; virus immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulne; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine gene therapy; vaccine; ; virucide; vulnerary; ds.

WO200159063-A2 Homo sapiens

16-AUG-2001

31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 17-JAN-2001; 2001WO-US001334

02-MAR-2000 16-MAR-2000 17-MAR-2000 18-APR-2000 19-MAY-2000 07-JUN-2000 28-JUN-2000 07-JUL-2000 07-JUL-2000 11-JUL-2000 11-JUL-2000 11-JUL-2000 11-JUL-2000 11-JUL-2000 26-JUL-2000 26-JUL-2000 26-JUL-2000 2000US-0180628P. 2000US-0184664P. 2000US-0184350P. 2000US-0189874P. 2000US-019076P. 2000US-0198123P.

2000US-0205515P 2000US-0214886P 2000US-0214886P 2000US-0215135P 2000US-0216647P 2000US-0217487P 2000US-021748P 2000US-0217496P 2000US-0217496P 2000US-0217496P 2000US-0217496P 2000US-0217496P 2000US-0217496P

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2000US-0225267P.

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The invention relates to novel genes (ABA11004-ABA21534) and proteins (CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC (ABB14678-ABB18001) useful for gene therapy. The genes are useful in the nucleic acids, proteins, antibodies and (ant)agonists are useful in CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune CC anaemia, autoimmune thyroiditis, diabetes, autoimmune haemolytic cancers, autoimmune thyroiditis, diabetes, autoimmune haemolytic contentials autoimmune thyroiditis, diabetes, autoimmune haemolytic cardiovascular disorders such as myocardial ischaemias; (d) wound healing (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) confectious diseases such as viral, bacterial, fungal and parasitic confectious diseases such as viral, bacterial, fungal and parasitic confectious diseases such as viral, bacterial, fungal and parasitic confectious diseases auch as viral, bacterial, fungal and parasitic confectious diseases auch as viral, bacterial, fungal and parasitic confectious diseases auch as viral, bacterial, fungal and parasitic confectious diseases auch as viral, bacterial, fungal and parasitic confectious diseases auch as viral, bacterial, fungal and parasitic confectious diseases auch as viral, bacterial, fungal and parasitic
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17-NOV-2000
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Best Local
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71; Conser
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Pred. No. 0.0036;
0; Mismatches 31;
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2000US-0229509P
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Query Match
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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                           gene therapy or antisense-therapy). Identifying mutations in the genes gene therapy or antisense-therapy). Identifying mutations in the genes gene therapy or antisense-therapy). Identifying mutations in the genes coding for the antisens is useful for diagnosing a pathological condition. The DNAs, antisens and antibodies raised against the antisens useful for treating, preventing and/ or prognosing disorders related to the endocrine system or hormone imbalance or reproductive disorders, cancers of endocrine tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the hypothalamus and testes (e.g. vanishing testes syndrome), many examples of diseases and disorders are given in the specification. The present sequence is genomic DNA fragment form a gene encoding an endocrine antisen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                               The invention relates to cDNAs encoding novel human endocrine antigens a fragment having biological activity, a domain, an epitope, full lengt protein, variant, allelic variant or a species homologue of the cDNA antigen. The DNAs and polypeptides are useful for preventing, treating or ameliorating a medical condition when administered (e.g. b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treating, preventing and prognosing disorders related to the endocrine system including endocrine disorders, reproductive disorders, and gastrointestinal disorders and also for testing and detection e.g. diagnosis.
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 572; 558pp; English.
                                                               Sequence 532 BP; 124 A; 164 C; 121 G; 123 T; 0 U;
Local Similarity
les 73; Conserv
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2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
2000US-02501030P.
2000US-0251988P.
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2000US-0249244P.
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               4.8%;
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                   Score 49.6; DB Pred. No. 0.009;
                                DB 4;
     39;
                                  Length 532;
                                                                      0 Other;
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Matches

Conservative

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Mismatches

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Katagiri
                                                                                                                                                                                                                                                              The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to pathogenic infection. The present sequence was used to appear the interaction of the plant to pathogenic infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                        Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogenic infection for conferring pathogenic infection for viral infection
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                                                                                                                                                                                                                                                     illustrate the invention.
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                                                                              expression.
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                                                                                                                                                                                   Similarity
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                      TTCCAGATGGTGGGAACTGGAGAGAGCCCGGCACAGGCCCCGTGCAGGGAACCCCGAGGGC 293
                                                     GSCKRKKSKGGSWGKTCRRGARGGSGWSSGAKYKSGSWSKRMWMSSCGRSGCGRRSAYSR
YYGTSRKYGTYKKMTYYSASRCMRAYMTTSYSWACSSYTWCRSKRRSMMWKMMRKMRWSR
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F, Quan
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                                                                                                                                                                    4.8%; Score 49.4; DB 8; Length 2000;
9.4%; Pred. No. 0.015;
ative 294; Mismatches 295; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      one gene involved in plant resistance or response
for conferring resistance or tolerance to a plant
viral infection by determining or detecting plant
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ie Z, Zhu
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RESULT 10

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AAS32311;

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AAS32311;

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DT

17-DEC-2001 (first entry)

XX

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Human cDNA encoding a novel end

XX

DE

Human; endocrine antigen; ss; c

KW thyroid-active; adrenal-active;

KW antisense-therapy; antibody; en

KW reproductive disorder; endocrin

KW diabetes mellitus; adrenal glan

KW hyperthyroidism; hypothalamic d

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11-JAN-2000; 2000US-018065BP.

PR

24-FEB-2000; 2000US-018055BP.

PR

24-FEB-2000; 2000US-018059P.

PR

15-MAR-2000; 2000US-0199123P.

PR

11-MAR-2000; 2000US-025515P.

PR

11-JUN-2000; 2000US-021686P.

PR

10-JUN-2000; 2000US-021688P.

PR

10-JUN-2000; 2000US-021688P.

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10-JUL-2000; 2000US-021688P.

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11-JUL-2000; 2000US-02168P.

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thyroid-active; adrenal-active;
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08-NOV-2000;
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08-NOV-2000;
                   a fragment having biological activity, a domain, an epitope, full length protein, variant, allelic variant or a species homologue of the cDNA antigen. The DNAs and polypeptides are useful for preventing, treating or ameliorating a medical condition when administered (e.g. by gene therapy or antisense-therapy). Identifying mutations in the genes coding for the antigens is useful for diagnosing a pathological condition or a susceptibility to a pathological condition. The DNAs, antigens and
                                                                                                                                                                        The invention relates to cDNAs encoding novel human endocrine antigens
                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                     Isolated polypeptide for treating, preventing and prognosing disorders related to the endocrine system including endocrine disorders, reproductive disorders, and gastrointestinal disorders and also for testing and detection e.g. diagnosis.
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      for treating,
      preventing
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Or.

expression

of the

receptor protein, and

as

immunogens to raise

Novel isolated G-protein coupled receptor peptide useful for treating disorder characterized by absence of, inappropriate or unwanted

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RESULT 11
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                                                                                 Gan
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                                                                                                                                                                                                                                                                                                                                                                               Key
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                                                                                                                                                                                                                                                                                                                                                                    variation
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)B; ABB81539.
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ilarity 64.3%;
Conservative
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replace(2182,T)
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                                                                                                                                                                                                                                 standard_name= "single nucleotide polymorphism
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1; Mismatches 39;
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RESULT 12
ADA71938/c
ID ADA719;
XX ADA719;
XX Plant;
AC Plant;
XW Gene;
XX OYZA
XX PO2003
XX PO2003
XX WO2003
XX O3-JAN
XX PF 22-JUN
XX Chang
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PI Katagi
XX WPI; 2
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Katagiri
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    The present involved in
                                                                                                                                      pathogenic infecti
bacterial, fungal
                                                                                                                                      Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAAGTAGATAATATTTTTATCTCCATTTTGCAAGAGATGAAGCTGAGGTCTAGAAAGG
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  invention relates to a method (M1) for identifying plant resistance or response to pathogenic infection
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RESULT 13
AALO5121/c
ID AALO51
XX
AC AALO51
XX
DT 21-NOV
DT 21-NOV
DX
XX
XX
XX
XX
XX
XX
BE Human;
XX
KW Cancer
XX

21-NOV-2001 AAL05121 AAL05121

(first

entry

standard;

DNA;

29163

ВÞ

cancer; gene

Human; reproductive system related

antigen;

reproductive

system

disorder;

therapy;

Human reproductive system

related antigen

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises identifying a gene whose expression is significantly altered the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infectio or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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111
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                                                                                               TGCCCACTGGGCATAGGCCTCTGGGAGCTGGCAGCATCGTGATCTCACTGATGCACCTGG
                                                                                                                                                                                                                                                                  SYKKKYCTWWCYMKCMRCYRWRKMMRKKTKYSKRCYCWRYATCYWCCCYRKRGWYSRRSM
                                                                                                                                                                                                                                                                                                                                 MGSYKYSRCYKYM-RMYMYKGWMYMMYYSAYSSMMTWYYYYAKYWKYWYKRRGTMSWYGK
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SYYKCYYĆYĆYWYMSYMR
                              CCCTTCCCGCCAGCGCAG 1038
                                                               YGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSMCCKKYCSCCTKYCSYTGYYRYCKWYKY
                                                                                                                                SRRAKMMRACRMYSACRRYSRTSYYCGCSYCGSSKWKYMSKSCSMRMTCSSWCSCCYTCY
                                                                                                                                                                AGTGTGGGCTGAGGCTCTGAACTGGGACAGGGGTCTCAGGAAGAGCCTCCTCCTCC
                                                                                                                                                                                                 MRTAGKWKMRSWSRWCRSYSWYKMYKKMWKKSYYMSYGWARSSGTWSRSAAKRTYKGYST
                                                                                                                                                                                                                                 CCCTTCCCAAATGCCTGCTGTCACTGCACTGCTGTGGTAGGGGGTCCCCAACGGGCTC
                                                                                                                                                                                                                                                                                                GCTCACGGCAATATCCTAACCTCTCTGAGCCTCCTGCCCAGCCTAGCAGGGTCCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAACAGACAAGGCCCAGGGGGACTAACCCGAGATCCAGCCCCGGCCTCACTCCCGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRAKRSYRYRRRWYWKRKGWTYRYRYWRSCRMTRARMSKRRKWAGASMKSCWMYWRGARS
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2000US-0231244P. 2000US-0231413P. 2000US-0231414P. 2000US-0232080P. 2000US-0232080P. 2000US-023296P. 2000US-0232397P. 2000US-0232397P. 2000US-0232399P.	2000US -0179065P. 2000US -018664P. 2000US -0186350P. 2000US -0186350P. 2000US -018913P. 2000US -019913P. 2000US -0219513P. 2000US -0216667P. 2000US -0216667P. 2000US -0216680P. 2000US -0217487P. 2000US -0217487P. 2000US -0217487P. 2000US -0225264P. 2000US -0225213P. 2000US -0225213P. 2000US -0225213P. 2000US -0225213P. 2000US -0225214P. 2000US -0225266P. 2000US -0225268P. 2000US -0225270P. 2000US -022576P. 2000US -022576P. 2000US -022578P. 2000	A2. 2001WO-US001339.
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RESULT 14
ABL98013/C
ID ABL98013 standard; DNA; 29163 BP.
XX
AC ABL98013;
XX
DT 21-JUN-2002 (first entry)
XX
DE Human; testicular antigen encoding D)
XX
Human; testicular antigen; testes; crapitator;
XW
reproductive system disorder; respirator;
XW
cardiovascular disorder; respirator;
XW
Gastrointestinal disease; infection
XX
WO200155317-A2.
XX
PN WO200155317-A2.
XX
PD 02-AUG-2001; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 04-FEB-2000; 2000US-0186350P.
PR 04-FEB-2000; 2000US-0186350P.
PR 17-MAR-2000; 2000US-018974P.
PR 17-MAR-2000; 2000US-018974P.
PR 18-APR-2000; 2000US-02515P.
PR 19-MAY-2000; 2000US-0216647P.
PR 28-JUN-2000; 2000US-0216647P.
PR 28-JUN-2000; 2000US-0216647P.
PR 30-JUL-2000; 2000US-021664P.
PR 11-JUL-2000; 2000US-0220963P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system related actives. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29163
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       2000US-0241787P.
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08-NOV-2000;
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                                                                                                                           reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding
                                                                                                                                                           The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system,
                                                                                          Sequence
                                                                                                                especially testicular cancers. The protein fragment of the invention
                                                                                                                                                                                                                                Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
                                                                                                                                                                                                                                                                    WPI; 2001-483232/52.
                                                         Local Similarity
                       51
                                              68;
                                                                                                                                                                                                                                                                                                                  HUMAN GENOME
                    AGGAGGCATATTCAGTCCCATTTTTCAGATGAGGAGTTGAGGCCCCAGAGAACGTAAGTA
                                                                                          29163
 AGGTGAGTGTTGTTATTCCCATTTTACAAATGAGGAATTGAGGCTCAGAGAGGGTGAAATT 8824
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2000US-0246528P.
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                                              Conservative
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                                              Score 48.2; DB 4;
Pred. No. 0.066;
0; Mismatches 33;
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49680 CAGGCTTTCCCATTTGCTACTCGCAGATACCCTAGACTGGCATAGTTACTGCCATTTTAT

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CAGTCCTCCACACTCAGTTCCCCACAGATGTGGTAGGAGGGCATATTCAGTCCCATTTTTC

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RESULT 15
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                                                                                                                                         The invention relates to recombinant carcinoma associated (CA) nucleic card sequences from mouse and human (ADA01482-ADA03094), and to CC recombinant carrinoma associated proteins (CAP) encoded by them. The cinvention also encompasses expression vectors and host cells comprising a CC Anucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a CC gathogenic trans-acting viral genes, meaning that cancer incidence is a CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of carcinoma by determination of the sequence of the invention. Note: The complete sequence data for this carcinoma compart of the printed specification, but was obtained considered to in electronic format directly from WIPO at the printered specification, but was obtained considered to carcer considered to carcer cancer are cancer as a specification, but was obtained considered to cancer c
Query Match
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Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
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                                                                                 Sequence 52661 BP; 15800 A; 11001 C; 11082
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Search Job ti	В	ş	Ф	Ş
Search completed: June 29, 2005, 15:39:57 Job time : 682 secs	49800 AAATGGATGTTGAACTGAAGTCTAGCTGTTTACAAAGCCCAGTC 49843	138 GCAGCCAGGCCCAGCCGAACCCCTGGTGTGTGCAGCCCCCAGCC 181	49740 AGATAGGTTCAAAGGTCCCCAAAATAATAGTGACTTGCCCCAAGGTCACACAGCTAGTGG 49799	78 AGATGAGGAGTTGAGGCCCAGAGAACGTAAGTTAATCTGTCTG

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Result
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## ALIGNMENTS

US-09-949-016-13793/c ; Sequence 13793, Application US/09949016 ; Patent No. 6812339

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GENERAL INCOMPATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMÓRPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
APRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13793
LENGTH: 72455
TYPE: DNA
RESULT 2
US-09-949-016-12115/c
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; Patent No. 6812339
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NAME/KEY: misc feature
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Pred. No. 4.6e-05;
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: WEI, MING-HUI et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001063
                                                                              Query Match 5.4%;
Best Local Similarity 70.1%;
Matches 89; Conservative
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LENGTH: 111282
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NAME/KEY: misc_feature
LOCATION: (1)...(104475)
OTHER INFORMATION: n = A,T,C
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CURRENT FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 5
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1)...(111282)
OTHER INFORMATION: n = A,T,C or
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  93162 TCCCCATTTTCAGGTGTGAAACTGAGGCCCAGAGAGGGTTTAGTGACTTGCTCAAGGTCAC
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                                 5.4%;
llarity 70.1%;
Conservative
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                                                                              Score 55.8; DB 3;
Pred. No. 5.5e-05;
0; Mismatches 37;
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Pred. No. 5.4e-05;
0; Mismatches 37;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTUARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15524
LENGTH: 256176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/331,498
PRIOR APPLICATION NUMBER: 60/331,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 12822
LENGTH: 256171
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US-09-949-016-15524/c
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Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: (1)...(256171)
OTHER INFORMATION: n = A,T,C
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72.2%;
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Pred. No. 0.0036;
0; Mismatches 2
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, NAME/KEY: misc_feature
; LOCATION: (1)...(256176)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15524
                                                                                                                                                      US-09-621-976-14118/c
                                                                                                                                                                             RESULT 7
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US-09-949-016-16177
                                                                                                 GENERAL INFORMATION:
                                                                                                                  Sequence 14118, Application US/09621976 Patent No. 6639063
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SEQ ID NO 16177
LENGTH: 24817
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Best Local Similarity
APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y. TITLE OP INVENTION: ESTs and Encoded FILE REPERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                  TAAGGCACAGAGCAGTTAAGAAAGTTGCCAGAGGTCACACAGCTAATAAGTGGTCGTTCC 7236
                                                                                                                                                                                                                                                                                                                                                                                             ACTCAGAACATAGACATGAGACAGGTACAATTATTTACCCAATTATTCATGATGGTGAAC 7176
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55.8%;
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72.2%;
                    and Encoded Human Proteins
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Pred. No. 0.0057;
0; Mismatches 72;
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Pred. No. 0.0036;
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OF DETECTION AND USES THEREOF
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RESULT 9
US-09-949-016-17033
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; ORGANISM: Homo sapiens
US-09-621-976-14118
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US-09-949-016-17032
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Sequence 17033, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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SOFTWARE: FastSEQ for
SEQ ID NO 17032
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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SEQ ID NO 14118
LENGTH: 473
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Best Local
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
83; Conserv
                                                                                                                                                                                                                                                                               GGCCACACAGCTAGAAAGCAGCC 143
                                                                                                                                                                                                                                                                                                                 CAGGTCAGGGAGCTTATATCCCCCTGCTTTCACACTCACAGCAACCCTGCAGAGTAGGAGT
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Pred. No. 0.0016;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 4;
Pred. No. 0.023;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 194937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                   60;
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S OF DETECTION
 ASSOCIATED OF DETECTION
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                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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   AND USES THEREOF
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FILE REFERENCE: CL001307

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-37,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 184953
LENGTH: 601
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US-09-949-016-184953
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17033
LENGTH: 194937
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 184953,
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Best Local :
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-949-016-17033
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                       82 GAGGAGTTGAGGCCCAGAGAACGTAAGTAATCTGTCTGAGGCCACACAGCTAGAAAGCAG 141
                                                                                                                                                                  22 CCTCCACACTCAGTTCCCACAGATGTGGTAGGAGGGCATATTCAGTCCCATTTTTCAGAT 81
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                                             GAGGAATCAAAGCTCAGAGAGGGTTAAATAACTTGCCTAAGGCCACACAGCAGGACTGCAG
                                                                                                                                  CCTGCTTTCACACTCACAGCAACCCTGCAGAGTAGGAGTGACTATTCCCATTCTTTAGAT
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                                                                                                                                                                                                                       Conservative
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58.0%;
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61.5%;
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                                                                                                                                                                                                                     Score 46.8; DB 4; Length 601; Pred. No. 0.0023; 0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 4; Length 194937;
Pred. No. 0.023;
0; Mismatches 60; Indels 0
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PATENT NO. 6812339

PATENT NO. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILTE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 16222
LENGTH: 43562
TYPE: DNA
CREATION HUMAN
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 185108
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(4352)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                             ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 CCTGCTTTCACACTCACAGCAACCCTGCAGAGTAGGAGTGACTATTCCCCATTCTTTAGAT 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.5%;
l Similarity 61.5%;
75; Conservariani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGAATCAAAGCTCAGAGAGGTTAAATAACTTGCCTAAGGCCACACAGCAGGACTGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09949016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46.8; DB 4;
Pred. No. 0.0023;
0; Mismatches 47;
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Query Match Best Local

Similarity

63.2%;

Length 43562;

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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-09-949-016-14371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: 1941247; PUBLICATION INFORMATION: US-09-313-300-6
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                                                                                                                                                                                                                                                                                                       Sequence 14371, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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SEQ ID NO 6
LENGTH: 703
TYPE: DNA
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APPLICANT: Baughn, Mariah, R.
APPLICANT: Baughn, Mariah, R.
APPLICANT: Azimzai, Yalda
TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
FILE REFERENCE: PB-0012 US
CURRENT APPLICATION NUMBER: US/09/313,300
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lal, Preeti
APPLICANT: Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kaser, Matthew, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.5%;
Local Similarity 67.2%;
les 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38106 CAACAACTCTATGAGATAAAAACAATTATTTCCATTTTACAGTCAAAGAATTGAGGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 CCACAGATGTGGTAGGAGGCCATATTCAGTCCCATTTTTCAGATGAGGAGTTGAGGCCCA 97
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAGGCACAGAGAGGTTAAGTGACTTGCCCCAAGGCCACACAGCGAGCCAGCGGTCAAGC 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46.8; DB 4;
Pred. No. 0.014;
0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                        ASSOCIATED
OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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; LENGTH: 57837
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14371
Search completed: June 29, Job time: 223 secs
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US-09-949-016-17601
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Best Local Similarity
Matches 81; Conserv
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Best Local Similarity 58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17601
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LENGTH: 57837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                     ACTGGCTCTCAGGCATGTG 20480
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US101_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US10 NEW PUB.seq:*
_6/ptodata/1/pubpna/US11 PUBCOMB.seq:*
_6/ptodata/1/pubpna/US11 NEW PUB.seq:*
_6/ptodata/1/pubpna/US10_NEW PUB.seq:*
_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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/pubpna/US06_NEW_PUB.seq:*
/pubpna/US06_PUBCOMB.seq:*
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S_PUBCOMB. seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

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49.6	49.6	52.4	52.4	55.8	1038	1038	Score
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710	532	7388	7086	111282	3006	3006	Length
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US-10-027-632-32570	US-10-074-024-572	US-09-764-891-5713	US-09-764-891-5712	US-10-094-989-3	US-10-617-443B-1	US-10-189-099A-1	DB ID
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US-10-461-862-4 US-10-027-632-288733	-10-027-632-1852	0-027-6	-10-027-632-1057	-10-027-632-10577	-10-719-993-6	0-087-192-4	-10-104-047-4	-10-719-993-4216	-10-027-632-1	-10-027-632-12737	-09-764-891-781	-10-719-993-690	-10-087-192-200	-10-741-601-561	-10-741-601-572	-09-997-722-298	-10-240-42	-09-997-722-142	-10-027-632-12285	-10-027-632-1228	-10-027-632-12285	S-10-027-632-12285	-10-027-632-13298	S-10-027-632 <b>-</b> 13298	-10-741-600-17650	S-10-027-632-22673	-10-027-632-22	-10-027-632-22673	S-10-027-632-22673	10-027-632-22673	-10-027-632-22673	-10-741-600-345	US-09-764-891-7809	ò	-074-024-	US-10-027-632-32570
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4, APP1: 288733,	8523,	18523, A	0577	0577	78,	466, App	436, App	e 42166, A	127376,	o.		6900, Ap	•		5726, Ap		1121, Ap		ທ	28	285	285	298	3298	7650	2673	226738,	26737	673	226738,	226737,	34521, A	7809, Ap	घ	71, Appl	32570, A

## ALIGNMENTS

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US-10-189-099A-1
                                                                                                                                                                                                                                ; TYPE: cDNA
; ORGANISM: Homo sapiens
US-10-189-099A-1
                                                                                                                                                                                                                                                                                               APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
FILE REFERENCE: ORT-1644
CURRENT APPLICATION NUMBER: US/10/189,099A
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10189099A Publication No. US20040005659A1 GENERAL INFORMATION:
                                                                                                                                         Matches 1038;
                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Darrow, Andrew L
APPLICANT: Qi, Jian-shen
APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon,
1 CAGGGACTCGAAGTTTGCAGTCCTCCACACTCAGTTCCCACAGATGTGGTAGGAGGGCAT
                                                1 CAGGGACTCGAAGTTTGCAGTCCTCCACACTCAGTTCCCACAGATGTGGTAGGAGGGCAT 60
                                                                                                                                    100.0%; Score 1038; DB 17; Length 3006; milarity 100.0%; Pred. No. 2e-305; Conservative 0; Mismatches 0; Indels 0;
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US-10-617-443B-1
; Sequence 1, Application US/10617443B
; Publication No. US20050019777A1
; GENERAL INFORMATION:
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; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Cailin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 ser
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/617,443B
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver: 2.1
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-617-443B-1
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Best Local Similarity
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Pred. No. 2e-305;
; Mismatches 0;
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Sequence 5712, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OP INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: WEI; MING-Hui et al

APPLICANT: WEI; MING-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001063DIV

CURRENT APPLICATION NUMBER: U$/10/094,989

CURRENT FILING DATE: 2002-03-12

PRIOR FILING DATE: 2002-03-12

PRIOR FILING DATE: 2002-03-12

PRIOR FILING DATE: 2002-03-03

PRIOR FILING DATE: 2002-03-03

PRIOR FILING DATE: 2007-04,989

CURRENT FILING DATE: 2002-03-12

PRIOR FILING DATE: 2002-03-12

PRIOR FILING DATE: 2007-04,989

CURRENT FARESPER OF SEQ ID NOS: 5

SOFTWARE: FASTSEQ for Windows Version 4.0
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Publication No. US20020115179A1
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LOCATION: (1)...(111282)
OTHER INFORMATION: n = A
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ORGANISM: Homo sapien
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Pred. No. 3.1e-06;
no. Mismatches 37;
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Best Local :
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                  ORGANISM: Homo sapiens
10-074-024-572
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-764-891-5712
Prior Application removed - See file Wrapper NUMBER OF SEQ ID NOS: 879
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 572
LENGTH: 532
TYPE: DNA
                                                                                                                                                                                                                         Sequence 572, Application US/10074024 Publication No. US20030232975A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior application data removed -
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5712
LENGTH: 7086
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SEQ ID NO 5713
LENGTH: 7388
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                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC001C1
CURRENT APPLICATION NUMBER: US/10/074,024
CURRENT FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 5.0%;
Local Similarity 69.6%;
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71; Conserv
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Pred. No. 2.2e-05;
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Pred. No. 2.3e-05;
0; Mismatches 31;
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/186,358
PRIOR APPLICATION NUMBER: US 60/186,358
PRIOR APPLICATION NUMBER: US 60/186,002
PRIOR APPLICATION NUMBER: US 60/186,002
PRIOR APPLICATION NUMBER: US 60/186,002
RESULT 8

US-10-027-632-32570
; Sequence 32570, Application US/10027632
; Sequence 32570, Application No. US20030204075A9
; Publication No. US20030204075A9
; GENERAL INFORMATION:
GAPPLICANT: Wang, David G.
; APPLICANT: WEARYION: Identification and Mapping of Single Nucleotide; TITLE OF INVENTION: Polymorphisms in the Human Genome
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108627.129
; FILE REFERENCE: 108627.129
; CURRENT APPLICATION NUMBER: US/10/027,632
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US-10-027-632-32570
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; NAME/KEY: misc_feature
; LOCATION: (1)... (710)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-32570
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 32570
LENGTH: 710
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 GTAGCTAGCAAGAAGCGGAGCCAGGACTCAACCTAAGTCTGAGCTCCTGCCA
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Pred. No. 0.00011;
0; Mismatches 39;
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Pred. No. 0.00011;
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR PELICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR PELICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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Publication No. US20030232975A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC001C1
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ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(710)
OTHER INFORMATION: n = A,T,C o
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. SEQ ID NO 71
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                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/074,024
CURRENT FILING DATE: 2002-02-14
Prior Application removed - See file Wrapper
NUMBER OF SEQ ID NOS: 879
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                                                                                                                                     OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (388)
                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (86)
OTHER INFORMATION: n equals a,t,9,
NAME/KEY: misc feature
LOCATION: (374)
                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                    OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (391)
OTHER INFORMATION: n equals
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              NAME/KEY: misc feature
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INFORMATION: n equals a,t,g, or
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78; Conservative
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No. US20030232975A1
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Pred. No. 0.00011;
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Sequence 7809, Application US/09764891

Publication No. US20030077808A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, an
FILE REFERENCE: PC006

CURRENT APPLICATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM o
                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7809
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SOFTWARE: FastSEQ for
SEQ ID NO 3
Query Match
Best Local Similarity
                                                                                                       SEQ ID NO 7809
LENGTH: 29163
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APPLICANT: GAN, Weiniu et al
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL001056
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                                                                                                                                           SOFTWARE: PatentIn Ver.
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CURRENT FILING DATE: 2000-12-20
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 7353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 GTAAGTAATCTGTCTGAGGCCACACACCTAGAAAGCAGCCAGGCCCAGCCGAACCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 ATGTGGTAGGAGGCATATTCAGTCCCATTTTTCAGATGAGGAGTTGAGGCCCCAGAGAAC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTAGCTAGCAAGAAGCGGAGCCAGGACTCAACCTAAGTCTGAGCTCCTGCCA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCCTTTTAGAGATGAAGGACTGAGGCTCAGAGAAGCCAAGTAATTCACYTAAGGCCAC 146
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   4.6%;
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Pred. No. 0.00021;
0; Mismatches 58
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Pred. No. 0.00014;
 Score 48.2; DB 10;
Pred. No. 0.00053;
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                Length 29163;
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CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34521
LENGTH: 201
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS C
                                                                            PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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TYPE: DNA
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RIOR APPLICATION NUMBER: US 60/146,002 RIOR FILING DATE: 1999-08-09
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                                         FILING DATE: 1999-09-28
                                                       APPLICATION NUMBER: US
                                                                                                                   APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTAACACCAAAGCCAGT 145
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Pred. No. 0.00029;
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITIE OF INVENTION: Identification and Mapping of Single Nucleotide
TITIE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,358
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
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; ORGANISM: Human
US-10-027-632-226737
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; Sequence 226738, Application US/10027632

; Publication No. US20020198371A1
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; ORGANISM: Human
US-10-027-632-226738
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Best Local Similarity 58.7%;
Matches 81; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 226738
LENGTH: 585
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Local Similarity 58.7%;
es 81; Conservative
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Pred. No. 0.00034;
1; Mismatches 56; Indels
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pred. No. 0.00034;
1; Mismatches 56
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1000-02-24
PRIOR PILING DATE: 1000-02-24
PRIOR PILING DATE: 1990-03-28
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
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US-10-027-632-226739
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Publication No. US20020198371A1

Publication No. US20020198371A1

GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE REFERENCE: 108827.129
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Search completed: June 29, Job time: 762 secs
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LENGTH: 585
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CURRENT FILING DATE: 2002-04-30
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd

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Result
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AL119782
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AL119782 DKFZp761F
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IL5-MT020
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CH240_17D
tigr-gss-
pan trog1
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wl84h03.x
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857546 MA
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HS_4554_A
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## ALIGNMENTS

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TITLE
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COMMENT
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   Best Loc
Matches
                 Query Match
Best Local 9
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German Genome Project.

No sl sequence available.

This clone (DKFZD761H1124) is available at the RZPD in This clone (DKFZD761H1124) is available at the RZPD in This clone (DKFZD761H1124) is available at the RZPD in This clone (DKFZD71H124) is available at the RZPD in This clone (DKFZD71H124) is available.
   89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A2119813
AL119813
DKFZD761H1124_r1 761 (synonym: h
DKFZD761H1124_5', mRNA sequence.
AL119813
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   Similarity
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   Conservative
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/tissue_type="amygdala"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: Not1;
                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                                                                                         organism="Homo sapiens"
|mol_type="mRNA"
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                   5.4%;
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 Score 55.8; DB 1
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0; Mismatches 3
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                                                                                   127
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                                                                                                                                           67
                                                                                                                                                                      89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                458 bp mRNA linear EST DKFZp761F1124_r1 761 (synonym: hamy2) Homo sapiens cDNA DKFZp761F1124 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                 This clone (DKFZp761F1124) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST (Bloecker, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             No s1 sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloecker, H., Boecher, M., Brandt, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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CCATCTT 153
                          TGCTCAT 192
                                                                        CCATCTT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAGCTCAAAAGCAGCAAAGCCGAAGCTGAAACCCAGGTCTGTCCAGCTCCCTGGCCAGG
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                                                                                                               TCCCCATTTTCAGGTGTGAAACTGAGGCCCAGAGACGTTTAGTGACTTGCTCAAGGTCAC
                                                                                                                                          TCCCCATTTTCAGGTGTGAAACTGAGGCCCAGAGACGTTTAGTGACTTGCTCAAGGTCAC
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                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="DKFZp761F1124"
/clone="DKFZp761F1124"
/tissue_type="amygdala"
/dev stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                      /clone_lib="761 (synonym: hamy2)"
/note="Vector: pSport1; Site_1: Not1; Site_2: SalI"
                                                                                                                                                                                  5.4%;
                                                                                                                                                                      0,
                                                                                                                                                                    Score 55.8; DB 1
Pred. No. 0.0027;
0; Mismatches 3
                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                       37;
                                                                                                                                                                                               Length 458;
                                                                                                                                                                       Indels
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TITLE
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Best Local S
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gooegawa and Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           854 NASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRCGGSGGASASHSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         914 SSBSCSSSSMSTSSSNSSBCSSCSSSBSSSSTSSMSSSSBSSSSSSSSSSSSSGTSSACVKC
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AL053013
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                             ACAAGGCCCAGGGGACTAACCCGAGATCCAGGCCCCGGCCTCACTCCCGTGTGGCTCACG
                                                                                                                                                                                                                                                                                                                                                                                             GCCCATGAGGAGAGGGCCAGTTCTCTCTCTGTAAGGGTATTGCTGTAGCATGAGGGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCCACTACACCCCCGCCTGGACACTGCTGTAGCCCCAGGGCTCGGAGGGACCAGCTGGA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCCAGAGGGGCCACGCTGTGTCCGGGCCTGGGTAGCTCAGAAGGGTCACCTGGGGGTC 547
GCAATATCCTAACCTCTCTGAGCCTCCTGCCCAGCCTAGCAGGGTCCAGTGAGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Drosophila melanogaster"
|mol_type="genomic_DNA"
|db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.3%; Score 54.8; DB 9; 16.5%; Pred. No. 0.0057;
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RESULT 5
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BE099553
383 bp mRNA linear 1
UI-R-BJ1-atj-f-11-0-UI.81 UI-R-BJ1 Rattus norvegicus
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Plate: 4554 row: O
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ808226 547 bp DNA linear GSS 10-AUG-1999
HS_4554_A2_H04_T7A CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=4554 Col=8 Row=0, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahairas, C.C., Wallace, J.C., Smith, K., Swartzell, S., Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                  TGCAGCCCCCAGCCCAGT 185
                                                                                                                                                                     GAAATTTACCCATGGTCACAAAGCTAGTGAGTAGTGAGCTCAAATCCAAACCCAGGTATG
                                                                                                                                                                                                    GTAATCTGTCTGAGGCCACACAGCTAGAAAAGCAGCCAGGCCCAGCCGAACCCCTGGTGTG 167
                                                                                                                                                                                                                                     GGTAGGAGGGCATATTCAGTCCCATTTTTCAGATGAGGAGTTGAGGCCCCAGAGAACGTAA 107
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="Plate=4554 Col=8
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                                                                                                                                                                                                                                                                                                     Score 51.6; DB 8;
Pred. No. 0.034;
0; Mismatches 54;
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111 ATCTGTCTGAGGCCACACAGCTAGAAAGCAGCCAGGC 147
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                                                                                                                                              68;
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Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the Notl Site and the oligo-dT track served to identify it as a clone from the normalized ventricle at 16.5 dpc library cDNA Library Preparation M.B. Soares Lab Clone distribution: clones will be available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UI-R-BJ1-atj-f-11-0-UI 3', mRNA sequence. BE099553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coordinated Laboratory
University of Iowa
375 Newton Road , 4156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
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                                                                                                                                                                 Similarity
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                                                                                AGGAGGGCATATTCAGTCCCATTTTTCAGATGAGGAGTTGAGGCCCCAGAGAACGTAAGTA 110
                                              AGGTGGTCATTTTATTCCCATTGTCTAGTTGAGAAACAGAGGCTCAGAGAAGCCAAGTG
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                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="UI-R-BJ1"
/note="Vector: pT713D-Pac (Pharmacia) with a modified
/note="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJ1
library is a subTracted library derived from the following
tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,
AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.
For a detailed description of the library from which this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soares, MB
                                                                                                                                                                                                                                                                                                                                                clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been pleaseribed in (Bonaldo, Lennon and Soares, Genome
                                                                                                                                                                                                                                                          TAG_TISŞUE=ventricle at 16.5 dpc
TAG_LIB=UI-R-BJ1
TAG_SEQ=GTTCG"
                                                                                                                                                                                                                                                                                                                                   6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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lab_host="DH10B (Life Technologies)"
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                                                                                                                                         Score 50.6; Di
Pred. No. 0.05
0; Mismatches
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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CE070706 536 bp DNA linear GSS 2 tigr-gas-dog-17000323019295 Dog Library Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Womack, J.E., de Jong, P.J. and Lewin, H.A. Bovine BAC end sequences from CHORI-240 library Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CRREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative)
Plate: 17 row: D column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
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CH240 17D11.TV CHORI-240
genomic survey sequence.
CC773356
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Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC773356.1
GSS.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
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                                                                                                                                                          AGGAGCCCGAGTCGCTG 217
                                                                                                                                                                                                         CGAACCCCTGGTGTGTG 169
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                                                                                                                                                                                                                                                                                                                                                              AGCTTGCACCGACCTCGTGAGAAACGTAATGTTAGCCCCATTTTACAGATGAGGAACTGAG
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ss: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ceil_type="Blood"
/cein_type="Blood"
/clone lib="CHORI-240"
/clone lib="CHORI-240"
/notee="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/notee="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/notee="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/notee="Vector: pto-1" | MboI; Site_2: MboI;
/notee: pto-1" | MboI; Site_2: MboI; Site_2: MboI;
/notee: pto-1" | MboI; Site_2: MboI; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
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/sex="Male"
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                               GSS 24-SEP-2003
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AUTHORS
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                          2 (bases 1 to 689)
Fujiyama, A., Hattori, M.
Totoki, Y., Watanabe, H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                    AG113318 689 bp DNA
Pan troglodytes DNA, clone: PTB-119015.R,
AG113318
AG113318.1 GI:16733837
     Submitted (02-AUG-2001) Asao Fujiyama,
                                                                                                                                                                                  Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                              Pan troglodytes (chimpanzee)
Pan troglodytes
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Class: shotgun
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kirkness EF
The Institute for Genomic
Department of Eukaryotic G
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The dog genome: survey sequencing and Science 301 (5641), 1898-1903 (2003)
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Rusch,D.B., Delcher,A.L.,
Venter,J.C.
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Canis familiaris
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                                                                                                                               Unpublished
                                                                                                                                                          BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Dog Library"
/note="Site_1: BstXI; Libraries were prepared
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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                                                                               Hattori, M.,
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Pred. No. 0.089;
0; Mismatches 5!
                                                       and Sakaki,Y.
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                                                                               Taylor, T.D.,
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CC552420/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245
Email: roll@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering.information.htm). This work

was underraken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 CAGATGTGGTAGGAGGGCATATTCAGTCCCATTTTTCAGATGAGGA-GTTGAGGCCCAGA 99
                                                                                                                                                                                                                                                                                                                Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A. Teai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Butterfield,Y., Kirkpatrick,R., Liu,J., Gud,R., Chan,A., Cl Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S., Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.M. Bovine BAC End Sequences from Library CHORI-240, PLATES 399 Unpublished (2003)
Other GSSs: CH240 438G3.T7
Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            790 bp DNA 1 CH240_438G3.TARBAC13P2 CHORI-240 Bos taurus CH240_438G3, genomic survev semianno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                            The British Columbia Cancer Agency (600 W. 10th Ave, Vancouver, British Tel: 604-877-6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
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                                                                                                                                                                                                              604-877-6276
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R.Site 1
R.Site 2
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/clone_lib="PTB Chimpanzee Male BAC Library"
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db_xref="taxon:9598"
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72.2%;
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n Columbia, Canada V5Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA sequence: 174-405, -MIR#SINE/MIR (matched compliment) Seq primer: M13 FORWARD POLYA-Yes.
                                                                                                     Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 97044477
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1 (bases 1 to 667)
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                                                                                                                                                                                                                                                      Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                                                                                                                                                  2024 University
                                                                                                                                                                                                                                                                                                                    University of Iowa
                                                                                                                                                                                                                                                                                                                                            McCray Lab
                                                                                                                                                                                                                                                                                                                                                           Contact: McCray,
                                                                                                                                                                                                                                                                                                                                                                                   8889548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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CB321964.1 GI:28856622
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/clone_lib="CHOR1-240"
/clone="Vector: pTARBAC1.3; Site_1: MboI; Site_2:
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2:
Hereford_bull_Li_Domino_99375; CHOR1-240_Bovine
library (Male)_produced_by_Pieter_de_Jong"
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/strain="breed: Hereford"
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                                                                                                                                                                   Unpublished (1997)
Other GSSs: RPCI-11-196N2.TJ
Other GSSs: RPCI-11-196N2.TJ
Other GSSs: RPCI-11-196N2.TJ
Contact: Shaying Zhao, William Nierman, Ma
Contact: Shaying Zhao, William Nierman, Ma
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 208
Tel: 301 838 0208
Fax: 301 838 0208
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1 (bases 1 to 454)
Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
AQ415695
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: T7
Class: BAC ends.
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of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="UI-CF-FN0-aem-m-06-0-UI"
/tissue type="Human Lung Epithelial cells"
/lab host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-CF-FN0"
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o sapiens genomic clone RPCI-11-196N2,
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                                                                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact pieter de Jong
quieter@dejong.med.buffalo.edu). Clones may be purchased from
gACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: T7
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AQ237490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other_GSSs: RPCI11-69K22.TJ
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301 838 0200
Fax: 301 838 0208
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Mammalia; Eutheria; Primates;
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/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
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/db_xref="GDB:7575193"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
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                                                                                                                     /mol_type="genomic DNA
/db_xref="GDB:7526373"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                    'sex="Male"
                                                                                     clone="RPCI-11-69K22"
                                                                                                                                                                                                                                                        organism="Homo sapiens"
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58.7%;
_type="Lymphocytes"
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Best Local
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                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                             198
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
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AL053013
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                              /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                       099-007-All&t3=1999-10-29&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL5-HT0207-291
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IL5-HT0207-291099-007-A11 HT0207 Homo sapiens cDNA,
BE145776
BE145776.1 GI:8608500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSASGSGSWSAGGGSGSTGSTSSSSSSSTSTSSSSVSSGSKSSTBSSGSBSSSGSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGSGSGS 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCACGC 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSSDSTSTCCSCCCYMCTCCSTYBMBCYTSTSCGGSSSSSGKGGVTKCGCGGCGSSSTN 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSSBBSCTSTSSSSSSSSSSSSTCSCCTCCCSYSYSSSTSSSSSTSWGSTSGSSSSSSVGT 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCCCGGCACAGGCCCGTGCAGGGAACCCCGAGGGCTGTAGGCCCCGTGCCACTGCATGC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTAGACACAGATGTAGGGCCCTGTGGACTCAGAAATTGGCAGCTCTTTTGGCCCCAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGGAAGGGTCCAGGGAAGTTCGTGAACCATCTAGCAAGTCGGGCTGGGGGTGTGGCCAA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCAGGCCTGTGGTCCTGGCAGCCACAGCCCCTACTGCTGACGGCAGCAGGAATCTGAGC 377
                                                                                                                                                                                                                                                                                               quality sequence stop: 150
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                              /db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                             clone
                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                          .150
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                                                                                                                                                                                                             type="mRNA"
                                                                                                                                           lib="HT0207"
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BI028582/c
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Best Local S
Matches 61
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Query Match 4.5%;
Best Local Similarity 75.3%;
Matches 58; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AGGAGGGCATATTCAGTCCCATTTTTCAGATGAGGAGTTGAGGCCCCAGAGAACGTAAGTA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 422)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bardin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI028582 422 bp mRNA linear IL5-MT0208-210201-356-f06 MT0208 Homo sapiens cDNA, BI028582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-MT0208-
210201-356-f66&t3=2001-02-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 320.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTTGTCCAAGGTCACACAGCAGGA 133
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                                                                                                                                                                      /organism="Homo sapiens"
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/mol_type="mRNA"
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/dev stage="Adult"
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/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
/note="Organ: puc18; Site_1: SmaI; Site_2: SmaI; SmaI; Site_2: SmaI; Site_2: SmaI; SmaI; SmaI; SmaI; SmaI; SmaI; SmaI; SmaI; Sma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
              Score 46.6; DB Pred. No. 0.64; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 andar, 01509-010, Sao Paulo-SP,
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                                                                                      DB 4;
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                         19;
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Search completed: June 29, 2005, 18:09:38 Job time : 4087 secs

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Result
No.
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-MODBLI-frame+_Dan_model _-DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10617443/runat_29062005_135931_26061/app_query.fasta_1.718
-DB=GenEmb1 _QFMT=fastap _SUFFIX=zge _MINMATCH=0.1 _LOOFCL=0 _LOOFSXT=0
-UNITS-bite _START=1 _END=-1 _MATRIX=bl0.sum62 _TRANS=human40.cdi _LIST=45
-DOCALIGN=200 _THR_SCORE=pct _THR_MAX=100 _THR_MIN=0 _ALIGN=15 _MODE=LOCAL
-OUTFMT=pto _NORM=ext _HEAPSIZE=500 _MINLEN0 _TMAXLEN=2000000000
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-NO_MMAP _LARGEQÜERY _NEG_SCORES=0 _WAIT _DSPBLOCK=100 _LONGLOG
-DEV_TIMEOUT=120 _WARN_TIMEOUT=30 _THREADS=1 _XCAPOP=10 _XGAPEXT=0.5 _FGAPOP=6
-FGAPEXT=7 _YGAPOP=10 _YGAPEXT=0.5 _DELOP=6 _DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                           Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                   Score
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Match
                                                                                                                                                                                                                                                                                                                                  GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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Ygapop 10.0 , X
Fgapop 6.0 , I
Delop 6.0 , I
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88.6
88.6
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AC113611 AC113611 AC113611 AC113611 AC113611.3 GI:28475761 HTG: Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata; V. Mammalia, Eutheria, Primates; Catarrhini; I (bases 1 to 60597) Suleton, J. E. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) 9903792 9847074 2 (bases 1 to 60597) Isak, A. and Cotton, M. The sequence of Homo sapiens BAC clone RP: Unpublished (2001) 3 (bases 1 to 60597) Waterston, R.H. Direct Submission Submitted (04-MAR-2002) Genome Sequencing University School of Medicine, 4444 Forest MO 63108, USA 4 (bases 1 to 60597)	39 88.6 117146 2 ACC087796 39 88.6 142401 8 ACC081865 39 88.6 150106 2 ACC144913 39 88.6 160650 3 ACC0018188 39 88.6 160650 3 ACC0018184 39 88.6 160850 2 ACC018184 39 88.6 218027 2 ACC137178 39 88.6 221049 2 ACC137179 39 88.6 2251586 2 BX957332 39 88.6 2251586 2 BX957332 39 88.6 2261586 2 BX957332 39 88.6 236192 2 ACC134753 39 88.6 236192 2 ACC134753 39 88.6 3 10654 3 AX4086427 31 86.4 19930 9 ACC00046 38 86.4 119903 9 ACC00046 38 86.4 119903 9 ACC091866 38 86.4 143298 8 ACC134240 38 86.4 157948 2 ACC124284 38 86.4 157948 9 ACC092532 38 86.4 162045 2 ACC124256 38 86.4 162045 2 ACC12512 38 86.4 170806 2 CR627483 38 86.4 177312 5 ACC126140 38 86.4 177312 5 ACC126140 38 86.4 179599 2 ACC110188 38 86.4 195090 2 ACC1102930 38 86.4 195090 2 ACC1102931 38 86.4 195685 2 ACC129372 38 86.4 195080 2 ACC129372 38 86.4 195080 2 ACC129372 38 86.4 195080 2 ACC129391 38 86.4 195080 2 ACC129972 38 86.4 195080 9 ACC00966 38 86.4 195090 9 ACC00723 38 86.4 195090 9 ACC00723 38 86.4 195090 9 ACC00723	
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                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
This sequence is not the entire insert of the clone. This clone
overlapped by AC104650 and AC104825.
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Submitted (10-MAR-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Feb 23, 2003 this sequence version replaced gi:20136967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 (bases 1 to 60597) Waterston, R.H.
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Direct Submission
Submitted (11-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                 Data from AC104825 was used to finish this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. 1 MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Contact: sapiens@watson.wustl.edu
----- Summary Statistics
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                      Direct Submission
Submitted (09-JUN-2001) Seattle Biomedical Research Institution, 4
Nickerson Street, Seattle, WA 98109-1651, USA
3 (bases 1 to 35546)
Worthey, E.A., Sisk, E., Seyler, A., Nelson, S., Vogt, C., Robertson, L.
Wellon, M., Ivens, A., Mack, J., Munden, H., Marty, A., Stuart, K. and
                                                                                                                                                                                                                                                                                                                                                                      35546 bp DNA linear INV 28-
Leishmania major chromosome 35 clone L4946 strain Friedlin,
complete sequence.
AC074202
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Myler,P.J., Sisk,E., Cawthra,J., Handley,F., Vogt,C., Robertson,L.,
McDonagh,P., Ivens,A., Nguyen,D., Munden,H., Stuart,K., Nelson,S.,
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                                                                                                                                                                                                Submitted (18-JUL-2000) Seattle Biomedical Research Institution,
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4 (bases 1 to 35546)
Worthey, E.A., Sisk, E.
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Pentony,M., Ivens,A., Mack,J., Munden,H., Marty,A., S
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/mol_type="genomic DNA"
/strain="Friedlin"
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chromosome="35"
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On Jan 16, 2002 this sequence version replaced gi:15778699.
*NOTE: This is a 'working draft' sequence. It currently
* consists of I contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 117146: contig of 117146 bp in length.
1 coation/Qualifiers
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Myler, P. J., Sisk, E., Cawthra, J., Handley, F., Vogt, C., Robertson, L., McDonagh, P., Ivens, A., Nguyen, D., Munden, H. and Stuart, K.
Direct Submission
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Myler, P.J., Sisk, E., Cawthra, J., Handley, F., Vogt, C., Robertson, L., McDonagh, P., Ivens, A., Nguyen, D., Munden, H. and Stuart, K. Direct Submission
Submitted (25-JAN-2001) Seattle Biomedical Research Institution, 4
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/mol_type="genomic DNA"
/strain="Friedlin"
                                                                                                                                                                                                                                                                               chromosome="35"/clone="9568"
                                                                                                                                                                                                                                                                                                                      db_xref="taxon:5664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117146 bp DNA linear HTG 14-APR-2003 major chromosome 35 clone P568 strain Friedlin, *** IN PROGRESS ***.
                                                                                                            1.1e+04
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88.89%
88.64%
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                                                                         AC087796 (1-117146)
                                                                                                                              Conservative: Mismatches: Indels:
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AC118669/c
   Percent Similarity:
Best Local Similarity:
                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The nucleotide sequence of this BAC clone was generated by combining Syngenta and Cold Spring Harbor Laboratory Genome Center sequencing data.

Clone OSJNBb0011G21 overlaps clone OSJNBb0085H08 (AC118340) from base 67378 (complemented) or OSJNBb0085H08 is from base 52004 to base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-SEP-2002) Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor, NY 11724, USA
On Sep 4, 2002 this sequence version replaced gi:20219081.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Shaughnessy, A., Palmer, L. and Dedhia, N. Genomic sequence for Oryza sativa, Nipponbare strain, clone OSJNBb0011G21, from chromosome 3, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                base 67378 to base 142401. The overlap 126708 (complemented) on OSUNBb0085H08.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-APR-2002) Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCombie, W.R., de la Bastide, M., Spiegel, L., Preston, R., Nascimento, L., Zutavern, T., Balija, V., Bell, M., Miller, B., Katzenberger, F., Muller, S., Sullivan, F., Yang, C., Dike, S., O'Shanghmaear a Balant S., Sullivan, F., Yang, C., Dike, S., O'Shanghmaear a Balant S., Sullivan, F., Yang, C., Dike, S., Sullivan, F., Yang, C., Sullivan, F., Yang, C., Sullivan, F., Yang, C., Sullivan, F., Sullivan, F., Sullivan, F., Yang, C., Sullivan, F., Sullivan,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct
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                                                                                                                                                                                                                                                       show one additional G assembly."
                                                                                                                                                                                                                                                                                                                       /note="We believe the assembly to be correct. The sequence is a mononucleotide (G) repeat in which the exact number of Gs is unknown. Four subclones in the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is a mononucleotide (C) repeat in wh
number of Cs is unknown. One subclone spans
into unique sequence on both sides."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="We believe the assembly to be correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="OSJNBb0011G21"
/clone_lib="EcoRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa
/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:39947"
chromosome="3"
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, Nipponbare strain, clone
complete sequence.
                                                                           142401
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US-10-617-443B-2_COPY_1_9 (1-9) x AC118669 (1-142401)
                                                                                                                     Birren, B., Nubbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Cooker, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelland, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Mendrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Ngyyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Nirect, Submission, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Submitted (21-JUL-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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1 (bases 1 to 150106)
Birren, B., Nusbaum, C. and Lander, E
                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research, 320 Charles Street, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-MAY-2003) Whitehead Institute/MIT Center
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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, WORKING DRAFT
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jul 21, 2003 this sequence version replaced gi:31074896. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                   108050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 127000; agarose-fp
Insert size: 148500; sum-of-contigs
Quality coverage: 10.9 in Q20 bases; agarose-fp
Quality coverage: 9.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 142901 bases at least Q40
Consensus quality: 146204 bases at least Q30
Consensus quality: 147399 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L29103
Center clone name: 203_A_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center Center code: WIBR
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                                                                 l_type="genomic DNA
_xref="taxon:10090"
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                                                                                                                                                 142079: gap of 100 bp
150106: contig of 8027 bp
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141979: contig of 19859 bp in length
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16543:
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AC008188/c
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Best Local Similarity:
Query Match:
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                                                                                    REFERENCE
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilae; Drosophila.

1 (bases 1 to 16059)
Celniker, S. E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
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BACR08118, (
AC008188
AC008188.4
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                                                                                                                                                                   Drosophila melanogaster (fruit
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21712. .2
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23370. .25160
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15714. .16443
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vector_side:right"
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28097. .30632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
25261. .27996
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1. .15613
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142080. .150106
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37569. .83287
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18701. .19955
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122121. .141979
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108150. .122020
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3388. .93357
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30733. .37468
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16544. .17157
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melanogaster, chromosome
complete sequence.
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Conservative:
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-JUL-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Apr 27, 2001 this sequence version replaced gi:6598785. Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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                                                                                                                                                        Drosophila melanogaster, AC018184
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                                                                                                                                                                                                                                                                                                                                              CACTTGGCATTGCCAGCCAGCGCC 81634
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/clone lib="RPCI 98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                          Plant Sciences, Athens, GA 30606, 2 (bases 1 to 167588)
Bastman, A.P., Smith, S.C. Borrer, Pratt T.
                                                                                                                                                                                                                      Plant Sciences, Athens, Georgia 30606, Sequence update by submitter On Jun 26, 2003 this sequence version Location/Qualifiers
                                                                                                                                                                                                                                                                          Submitted (26-JUN-2003) Botany, University Plant Sciences, Athens, Georgia 30606, USA
                                                                                                                                                                                                                                                                                                           Eastman, A.P., Smith, S.C., Bertin, N., Liang, C., Pratt, L.H. and Cordonnier-Pratt, M.-M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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/mol_type="genomic DNA"
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CE 3 (bases 1 to 196178)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Boode, S., Dooley, K., Dorris, L., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., O'liver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Vimer, A., and J., Zembek, L., Zimmer, A. and J., Can, M.X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Can, M.X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and J., Can, M.X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
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Birren,B., Nusbaum,C. and Lander,E.
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Direct Submission
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RS Birren, B., Musbaum, C., Lander, E., Abouelleil, A., Allen, V., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Cheppel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Erickson, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Noven, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., O'Iver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Vona, N., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Vanney, A., and John, J., Wall, R., Venkataraman, V.S., Viel, R., Vanney, A., Maran, D., Young, G., Zainoun, J., Zembek, L., Vanney, A., Maran, D., Young, G., Zainoun, J., Zembek, L., Vanney, A., Maran, D., Young, G., Zainoun, J., Zembek, L., Vanney, A., Maran, D., Young, G., Zainoun, J., Zembek, L., Vanney, A., Maran, D., Young, G., Zainoun, J., Zembek, L., Vanney, A., Wallson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Vanney, A., Wallson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Vanney, A., Vanney, G., Zainoun, J., Zembek, L., Vanney, A., Vanney, G., Zainoun, J., Zembek, L., Vanney, A., Vanney, G., Zainoun, J., Zembek, L., Vanney, A., Vanney,
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Center clone name: 179_A_6
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  1.76e+04
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100.00%
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7. .15213
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1. 21866
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[ement(19996
                                                                                                                                                                                                                                                                                                                                                               family="B1_MM"
[ement (1600]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family="L1ME2"
ement(1577)
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ement(15477)
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ement (14000
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Tement(13815. .13903)
_family="PB1D7"
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[ement(1)]
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≧MM"
                                        Length:
Matches:
  Mismatches:
Indels:
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                            Conservative:
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AC146955/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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Otolemur garnettii
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AC146955.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NISC Comparative Sequencing Initiative Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Green, E.D.
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HTG; HTGS_PHASE1; HTGS_
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                                                                              as soon as it is available and be preserved.
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 2403
2503
9515
9615
14217
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Contact: nisc_zoo@nhgri.nih.gov
----- project Information
                                                                                                                                                                                                                                                                                                                                 Center clone name: 263M09
                                                                                                                                                                                                                                                                                                                                                              Center project name: fkv
2402: contig of 2402 bp in length 2502: gap of unknown length 9514: contig of 7012 bp in length 9614: gap of unknown length 14216: contig of 4602 bp in length 14316: gap of unknown length
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US-10-617-443B-2_COPY_1_9 (1-9) x AC107764 (1-196178)
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Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B.,
Coleman, H., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurle, B., Idol, J.R.,
Han, J., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q.,
Karlins, E., Kwong, P., Laric, P., Larson, S., Lee-Lin, S.-Q.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Marguliss, B.H., Masiello, C.,
Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schandler, K.,
Schueler, M.G., Shah, K., Sison, C., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and
Green F. D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur 1 (bases 1 to 218827)
                                      NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; n/a; 100% of reads Chemietry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality; 213879 bases at least Q40
Consensus quality: 215076 bases at least Q30
Consensus quality: 21592 bases at least Q30
Consensus quality: 215592 bases at least Q20
Insert size: 234000; agarose-fp
Insert size: 217327; sum-of-contigs
Quality coverage: 9.95x in Q20 bases; agarose-fp
Quality coverage: 9.96x in Q20 bases; sum-of-contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center Center code: NISC
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the accession number
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sum-of-contigs
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FEATURES
          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                               Pred. No.:
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,40: contig of 6836 bp in length
,40: contig of 6836 bp in length
,40: gap of unknown length
,78: contig of 12047 bp in length
,78: gap of unknown length
,194: contig of 1097 bp in length
,5208: gap of unknown length
63590: contig of 11506 bp in length
63590: gap of unknown length
,73810: gap of unknown length
,73910: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
31741. .43787
                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
88105...107084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment" 63691. .73810
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14317. .24704
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/mol type="genomic DNA"
/db_xref="taxon:30611"
/clone="CH256-263M9"
                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
107185 .124220
/note="assembly_fragment"
124421 .145411
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|. .2402
                                                                                                                                                                                                   /note="assembly_fragment"
189368. 218827
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145512. .164902
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165003. .189267
                                  1.94e+04
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Matches:
                     Mismatches:
Indels:
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RESULT 13
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                                                                           Multry, D. Marie., Merzker, M. Lee, A. Angulano, D. Mallen, C. Allen, H., Alsbrooks, S., Angulano, D., Allen, H., Alsbrooks, S., Angulano, D., Anyalabechi, V., Aoyadi, A., Aydelji, M., Baca, E., Baden, H., Anyalabechi, V., Aoyadi, A., Aydelji, M., Baca, E., Baden, H., Anyalabechi, V., Aoyadi, A., Aydelji, M., Baca, E., Baden, H., Anyalabechi, V., Aoyadi, A., Aydelji, M., Baca, E., Baden, H., Barrisead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barrisead, M., Berand, D., Barber, M., Barrisead, M., Baca, E., Baden, M., Baland, C., Caderon, B., Bryant, M., Carter, W., Carezos, I., Casar, H., Cchen, C., Chen, C., Chen, C., Chen, C., Chen, Y., Chen, C., Chen, R., Chen, Y., Chen, C., Chen, Y., Chen, C., Chen, Y., Chen, C., Chen, R., Chen, Y., Chen, C., Chen, Y., Chen, Y., Chen, R., Chen, Y., Chen, Y., Chen, R., Chen, Y., 
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                 Direct Submission
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FEATURES
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TITLE
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misc_feature
                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequence and whole genome shotgun sequences will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.h
NOTE: This is a "working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                   215097
215197
216257
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Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 155203 bases at least (
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Consensus quality: 161146 bases at least Q30
Consensus quality: 165262 bases at least Q20
Estimated insert size: 159376; sum-of-contigs estimation
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10574
182910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
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    /note="wgs_contig"
61410. .63256
                                                                                                                                        organism="Rattus norvegicus"
/mol_type="genomic DNA"
                                                       note="wgs_contig"
                                                                                                 clone="CH230-unknown"
                                                                                                                     db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10473: contig of 10473 bp in length
10573: gap of unknown length
182909: contig of 172336 bp in length
                                                                                                                                                                                                                                       9653: gap of
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                                         17449
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53: contig
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contig
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of 1539
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BX957332
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Query Match:
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US-10-617-443B-2_COPY_1_9 (1-9) x AC137178 (1-221049)
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                                                                                                                                                                                                                                                                                                                                                             Submitted (09-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 10, 2004 this sequence version replaced gi:52694723.
                  Chemistry: Dye-terminator; 100% of reads Consensus quality: 220348 bases at least Q40 Consensus quality: 220544 bases at least Q30 Consensus quality: 220727 bases at least Q20 Insert size: 220053; 2.6% error; agarose-fp Quality coverage: 7.93x in Q20 bases; sum-of-
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HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
Danio rerio
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 221586)
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coverage: 8.01x in Q20 bases; agarose-fp
                                                                                                                                                                              Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                           Center project name: zK170K13
                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                     Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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99109 .101394
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116970. .119727
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74577. .75784
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134730. .136296
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88264. .189718
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175836. .177673
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|62057. .163329
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|12096. .113281
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96819. .99058
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39.00
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Indels:
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Matches:
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                     sum-of-contigs Quality
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Percent Similarity:
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                                                                                                                                                                                        RESULT 15
AC099140
                           ACCESSION
VERSION
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KEYWORDS
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                                                                                                                         AC099140 238103 bp DNA linear HTG 10-M
Rattus norvegicus clone CH230-52Al4, WORKING DRAFT SEQUENCE,
                                                              unordered pieces.
AC099140
AC099140.12 GI:30522132
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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fragment_chain:1"
113385. .121021
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-170K13"
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fragment_chain:1"
184203. .221586
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fragment_chain:1"
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162929: contig of 5962 bp in length
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184102: contig of 21073 bp in length
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221586: contig of 37384 bp in length.
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ractus.
                                                                                                                                                                                                                                                                                      Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 238103) TX RAI Genome Sequencing Consortium.
                        Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:23264508. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequencing reads assembled using Atlas and Whole genome shotgun sequence which who who who who were sequenced to the sequenced and whole genome shotgun sequenced to the sequenced 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
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FEATURES

US-10-617-443B-2_COPY_1_9 (1-9) x AC099140 (1-238103)

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172836 CATCTCGCCCTCCCTGCTTCCGCC 172859
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Search completed: June 29, 2005, 23:51:05 Job time: 337.461 secs

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Run on:

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       N_Geneseq_16Dec04:*
1: geneseqn1980s:*
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                                                                                                                                                                                                                                                                                                                                                                                                  human; PRSS11-L; gene; ss; S2 serine protease; S2/Ht cellular physiology; apoptosis; gene therapy; osteoa apoptotic; osteopathic; antiarthritic; tranquiliser.
                03-JUL-2002; 2002US-00189099
                                       03-JUL-2002; 2002US-00189099
                                                                                                                                                                                                                                         Human PRSS11-L cDNA encoding a serine protease SeqID 1.
                                                                                                                                                                                                                                                                                        ADJ11355;
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                 20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                              ADJ11355 standard; cDNA; 3006 BP.
                                                                                      US2004005659-A1
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AAV41533

AAV415947
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ADA27231
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AAC40009
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ADJ11359
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                                                                                                                                                                                                        osteoarthritis;
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Aca57488 Human adi
Adq65511 Human tum
Adq65511 Human pol
Aai59099 Human pol
Adi64918 Novel hum
Ada59932 DNA encod
Add49082 Novel hum
Aba01852 Human reg
Add121987 Novel hum
Aba01852 Human NOV
Add27231 Human NOV
Add27231 Human sen
Acc48788 Human Evi
Acc48788 Human Evi
Acc48788 Human Evi
Acc48792 Human Evi
Adc49028 Human NOV
Aac93383 Human NOV
Aac93383 Human NOV
Aac93383 Human NOV
Aac93583 Human NOV
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Adj11359 PCR prime
Ac124588 DNA clone
Aca22808 Prokaryot
Aca21959 Prokaryot
Add62510 A. thalia
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Aav41533 Nucleorid
Aav15947 Mouse syn
Aca60751 Mouse syn
Acn45004 Mouse gen
Aak67239 Human imm
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Ade95830 Human REL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel isolated nucleic acid molecule identified as PRSS11-L that encodes an $2 serine protease. Specifically, it refers to members of the $27/HtrA serine protease family, such that it plays a role in cellular physiology and apoptosis. The present invention provides agonists, antagonists, antibodies and recombinant expression vectors useful in methods of treatment, or detection and diagnosis of diseases associated with the aberrant expression or activity of the $2 serine protease, PRSS11-L. Accordingly, compositions described herein can be used via gene therapy routes to treat osteoarthritis, stress and apoptotic disorders. As such, they exhibit osteopathic, antiarrhritic and tranguilliser activities. This polynucleotide sequence is the human PRSS11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated S2 serine protease nucleic acids and polypeptides, useful for diagnosing and/or treating diseases with aberrant expression or activity the S2 serine protease, such as osteoarthritis, stress and
                           Hemmati-Brivanlou
                                                                                                                                                                US2002081610-A1
                                                                                                                                                                                                                     Frog; ss; embryonic development; developmental disorder; microarray;
cell differentiation.
                                                                               21-JUL-2000;
                                                                                                          23-JUL-2001; 2001US-00910943.
                                                                                                                                      27-JUN-2002
                                                                                                                                                                                          Xenopus laevis
                                                                                                                                                                                                                                                            Frog embryonic gene sequence Q9925836
                                                                                                                                                                                                                                                                                         12-DEC-2002
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DB; ADJ11356.
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CC sequences (appearing as ABS76747-ABS77516) a of a xenopus embryonic gene contriguous nucleotides of one of those sequences. Also included are contacting differential expression of embryonic genes, comprising: (a) contacting a nucleot acid array comprising genes expressed in embryonic but not mature cells with nucleic acids from sample and control cells; and (b) detecting differential hybridisation of nucleic acids from the sample cells relative to the control cells; and detecting defects in cells and control cells; and cevelopment, comprising: (a) contacting nucleic acids from the condergoing development with a nucleic acid array of gene products known to play a fundamental role in the development process; and (b) detecting a difference in expression of a fundamental gene in the sample cells relative to a standard. The invention is useful to identify genes involved in embryonic development and related processes such as cell differentiation. This would be useful for disgnosing developmental cells. The disorders and for identifying different types of embryonic cells. The present sequences is one of the 770 Xenopus embryonic cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid array containing Xenopus embryonic nucleic acids is useful to identify genes involved in embryonic development, to identify different types of embryonic cells, and to diagnose developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 698; 823pp; English.
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Query Match: RESULT 밁 S US-10-617-443B-2_COPY_1_9 (1-9) Alignment Scores: Pred. No.: grug 21-MAR 2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-QCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851. 21-MAR-2002; 03-OCT-2002. WO200277183-A2 Burkholderia fungorum. Prokaryotic Antisense; ds; prokaryotic essential gene; cell proliferation; 19-JUN-2003 ACA25538; ACA25538 standard; DNA; 963 design; 327 essential gene #7195. 2002WO-US009107 gene. (first entry) 2002US-0362699P 346 39.00 100.00% 77.78% 88.64% x ABS77428 (1-754) Length: Matches: Mismatches: Indels: Conservative: 9 754 0 0

(ELIT-) ELITRA PHARM INC

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a polypeptide whose expression is inhibited by the antisense conucleic acid; (2) a host cell containing the vector; (3) an isolated copolypeptide or its fragment whose expression is inhibited by the collection or the fragment whose expression is inhibited by the compounding companies; (5) producing the polypeptide; (6) inhibiting cellular compounding companies; (7) identifying a gene in an operon required for compounding the polypeptide; (8) product or that has an activity against a biological pathway compounded that influences the activity of compounding red for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies cor a gene on which the test compound that inhibits proliferation of an compounding acts; (9) manufacturing an antibiotic; (10) profiling a compounding acts; (9) manufacturing an antibiotic; (10) profiling a compounding activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compounding the cardinal for collection of confidention of an organism. The antisense nucleic acids are useful for clanifying proteins or screening for homologous mucleic acids required confidence collections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/muh/muhitemad ---
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Prokaryotic essential gene #7627.
                                                                                                              ACA25970;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhin
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                                                                                                                                                              ACA25970 standard; DNA; 2157
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Xu HH;
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Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

US-10-617-443B-2_COPY_1_9 (1-9) x ACA25970 (1-2157)

Best Local Percent Similarity:

Similarity:

88.89%

Conservative: Mismatches: Indels:

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CC encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated containing the polypeptide by the containing the polypeptide; (5) producing the polypeptide; (6) inhibited by the containing the polypeptide; (6) inhibiting cellular containing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway containing a gene required for cellular proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene contains acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene conduct is overexpressed or underexpressed; (12) determining the extent convolute activity; (13) identifying the target of a compound that inhibits the convolution of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required confidence and iscovery programs, or for screening processing nucleic acids are useful.
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 6213 antisense sequences given in the specification where expres
of the nucleic acid inhibits proliferation of a cell. Also included
(1) a vector comprising a promoter operably linked to the nucleic ac
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                                                                                                                                           form part of the printed specification, ctronic format directly from WIPO at
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                                                  Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
gene; ds.
                                                                                                                                                                                                                                                                                           06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                      ADA02582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA02582 standard;
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                                                                                                                                                                                                            Human REL
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                                                                                                                                                                                                                carcinoma associated gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 60940 BP
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Matches:
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The invention relates to recombinant carcinoma associated (CA) nucleic cc acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The cc invention also encompasses expression vectors and host cells comprising a cinvention also encompasses expression vectors and host cells comprising a cinvention also encompasses expression vectors and host cells comprising a cinvention are related to the protein, and a biochip comprising CA nucleic acid or comprising the tells comprising CC and tell thereof. The sequences of the invention were identified using creating the carcy transduced host oncogenes or carcinoma. Many of these do not carry transduced host oncogenes or cc at random. Many of these do not carry transduced host oncogenes or cc at random. Many of the effects of proviral integration into host cdirect consequence of the effects of proviral integration into host correct consequence. The CA nucleic acid sequences can be used to diagnose creations (especially breast cancer, prostate cancer, lymphoma or carcinoma (especially breast cancer, prostate cancer, lymphoma or composed com
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
RESULT 7
ADB72320/c
ID ADB723320/c
ID ADB7233
XX
AC ADB723
XX
O4-DEC
DT 04-DEC
XX
XX
DB Human
XX
human;
KW human;
XX
human;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2001; 2001US-00035832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60940 BP; 16572 A; 11094 C; 10947
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                                                                                                                                                                                                      ADB72320
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                                                                                                                                                                   ADB72320;
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human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.

Human

gene.

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Percent Similarity:
Best Local Similarity:
Query Match:
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23-OCT-2001;
08-NOV-2001;
30-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                      08-NOV-2001; 2001US-00052482
                                               08-NOV-2002; 2002WO-US036071.
                                                                                               WO2003039484-A2
                                                                                                                        Homo sapiens
                                                                                                                                                            cancer diagnosis;
                                                                                                                                                                                    Human REL gene genomic DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60940 BP; 16572 A; 11094 C; 10947 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 148; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid, useful for treating carcinomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                               lymphoma;
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                                                                                                                                                                                                                                       ADE95830
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(SAGR-) SAGRES DISCOVERY
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; 2001US-00052482.
; 2001US-00997722.
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                                                                                                                                                 cancer;
                                                                                                                                               cancer treatment; carcinoma; cytostatic; gene therapy;
cancer; prostate cancer; leukaemia; ds; human; REL.
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Best Local Similarity:
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                                           Sequence split
                                                                                                                                                                                                                                                                                                                                              lymphoma, breast cancer, prostate cancer or leukaemia, for example drug candidates or bioactive agents capable of binding to, for modulating the activity of, a carcinoma associated protein. The present sequence is the genomic DNA sequence of the human REL gene which is a carcinoma associated gene of the invention.
                                                                                                                                                                                                                                                                                                                            Sequence 60940 BP; 16572 A; 11095 C; 10946 G;
                                                                                                                                                                                                                                                                                                                                                                                                                               invention may have cytostatic activity whilst the disclosed sequences may be useful for gene therapy. The carcinoma associated nucleic acids and proteins are useful for diagnosing and treating carcinomas, for example
                                                                                                                                                                                                                                                                                  No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis and treatment of cancer, especially use of compositions in screening methods. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel recombinant nucleic acids for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 88; 793pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New carcinoma associated nucleic acids and proteins, useful drug candidates, or for diagnosing and treating carcinomas, lymphoma, breast cancer, prostate cancer or leukemia.
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RESULT 9
AAI199682 19/c.
Continuation (20 of 45) of AAI199682 from base 1900001 (Mycobacterium tuberculosis strain
Continuation (20 of 45) of AAI199682 from base 1900001 (Mycobacterium tuberculosis strain
WP Sequence split into 45 fragments LOCUS AAI199682 Accession Aai199682
WP AAI19682 01 100001 210000
WP AAI19682 02 200001 310000
WP AAI199682 03 300001 410000
WP AAI199682 04 400001 510000
WP AAI199682 06 600001 710000
WP AAI199682 07 700001 110000
WP AAI199682 0 900001 110000
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WP AAI199682 11 1100001 1210000
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WP AAI199682 15 1500001 1610000
WP AAI199682 16 1600001 1710000
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WP AAI199682 18 1800001 2100000
WP AAI199682 20 2000001 210000
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WP AAI199682 28 2600001 2810000

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RESULT 10
AAQ67901/c
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                Syndecan gene enhancer element.
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08-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                             No
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                                                                                                                                                                                         WO9412162-A1
                                                                                                                                                                                                       qa ap
                                                                                                   (WAER/)
(ALAN/)
(AUVI/)
(JAAK/)
(JALK/)
                                                                                                                                              01-DEC-1992;
                                                                                                                                                             01-DEC-1993;
      Disclosure; Page 40-41; 65pp; English.
                                                                                     (LEPP/)
                     Syndecan stimulation of cellul
tumour growth used to promote
                                          WPI; 1994-199926/24.
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                                                                 Waerri
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') ALANEN-KURKI L M.
') AUVINEN P O V.
') JAAKKOLA P M.
') JALKANEN M T.
') JALKANEN S M.
') LEPPAE S M.
') MALI M S.
') VIHINEN T A.
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                                                                                                                                                                                                                    enhancer; differentiation; tumor; therapy; hair growth;
                              stimulation
                                                        Alanen-Kurki LM,
Mali MS, Vihinen
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(first en
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                       of cellular differentiation promote hair growth.
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Alignment Pred. No.:

Percent Similarity: Best Local Similarit

Similarity:

2.7e+03 37.00 100.00% 87.50%

Length:
Matches:
Conservative:
Mismatches:

2196 7 1 0

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RESULT 11
AAV41533/c
ID AAV41533;
XX 28-SEP-19:
XX Nucleotide
XX Mouse; syr
XX Mouse; syr
XX Mouse sp.
XX Woond heal
XX Woond heal
XX Woond heal
XX WOODEC-19:
XX WO2-DEC-19:
XX (BIOT-) B]
XX (BIOT-) B]
XX WPI; 1998-
XX WPI; 1998-
XX New synder
PR WPI; 1998-
XX New synder
PR Disclosure
XX Disclosure
XX Disclosure
XX This is th
CC This is th
CC Cell for c
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XX Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The mouse syndecan gene enhancer, located 8-10 kb upstream from the initiation site, is given in AAQ67901. Manipulation of the enhancer can be used either to slow or prevent tumor growth or to promote differentiation of specific cell types, e.g. epidermal cells to promote hair formation. The complete mouse syndecan gene and its encoded protein are given in AAQ67902 and AAR55276. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2196 BP; 509 A; 582
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                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; syndecan gene; syndecan enhancer element; expression vector; wound healing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                              WO9824921-A1
                                       This is the nucleotide sequence of the mouse syndecan gene, used in the method of the invention involving the novel syndecan enhancer element, useful in expression vectors. The vector can be used to produce a host cell for expressing a structural gene. The expression vector can be used to differentially express a gene at a wound site, and promote wound
                                                                                                                                                                 New syndecan enhancer element
                                                                                                                                                                                            WPI; 1998-333338/29.
                                                                                                                                                                                                                                                                             02-DEC-1996;
                                                                                                                                                                                                                                                                                                          02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                   11-JUN-1998
                                                                                                                        pisclosure; Page 29-30; 57pp; English
                                                                                                                                                     promoting wound healing.
                                                                                                                                                                                                                                                    (BIOT-) BIOTIE THERAPIES
  Sequence 2196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetHisLeuAlaLeuProAlaSer 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA;
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                                                                                                                                                                                                                          Jaakkola P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
     B₽;
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                                                                                                                                                                                                                                                                                                            97WO-FI000748.
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37.00
100.00%
87.50%
84.09%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              of mouse syndecan gene.
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Matches:
Conservative:
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           569
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RESULT 12
AAV15947/c
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-1992;
01-DEC-1993;
07-MAR-1994;
        vectors which contain either the enhancing or suppressing DNA molecules. The products may be used to alter the differentiated state of a host cell by altering its expression of syndecan, e.g. to induce and regulate syndecan expression, especially in cells which exhibit a malignant phenotype, regardless of the origin of transformation. The products can be used to produce therapeutics for suppressing tumour growth. They may enhance the syndecan expression in a host cell, by enhancing its gene transcription, especially in malignant or normal cells, and therefore
                                                                                                                enhances the expression of a gene operably linked to the promoter of the mouse syndecan gene in 3T3 cells following treatment with TGP- beta and bFGF when the fragment is operably linked to the promoter. A purified DNA molecule comprising a portion of the nucleotide residues 3538-3888 of the mouse syndecan genomic sequence (AAVI5946) suppresses expression of a gene operably linked to the promoter of the mouse syndecan gene in S115 cells treated with testosterone. Host cells can be transfected with
                                                                                                                                                                                                                                                                                                    New mouse syndecan gene sequences -
                                                                                                                                                                                                          approximately 9 kb upstream from the transcription initiation site. A base pair fragment (AAV15948) of this purified enhancing DNA molecule
                                                                                                                                                                                                                                    This is the mouse syndecan gene
                                                                                                                                                                                                                                                              Claim 1; Fig 4; 48pp; English.
                                                                                                                                                                                                                                                                                                                                            WPI; 1998-192770/17
                                                                                                                                                                                                                                                                                                                                                                                 Jaakkola P,
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(MALI/)
(VIHI/)
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                                                                                                                                                                                                                                                                                                                                                                       Auvinen
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                                                                                                                                                                                                                                                                                                                                                                                                             (JAAK/)
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ALANEN-KURKI
LEPPAE S.
JAAKKOLA P.
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MALI M.
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Jalkanen M,
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94US-00206186
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Vihinen T;
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Gaps:
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                                                                                                                                                                                                                                                                                                    for, e.g. suppressing tumour processes such as wound
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ID ACA607
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AC ACA607
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Query Match:
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                    07-MAR-1994;
                             01-DEC-1993;
                                                  21-JUN-1999;
                                                                      10-DEC-2002
                                                                                         US6492344-B1
                                                                                                                                          misc_binding
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(BIOT-) BIOTIE THERAPIES CORP
                                                                                                                                                                                                                                                                                                                                                                                                               de an
                                                                                                                                                                                                                                                                                                                                                                                                                                   hair growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse syndecan enhancer element, FGF-inducible Response Element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              issue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1143
                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; syndecan enhancer element; cutaneous wound healing; FiRE;
regeneration; syndecan regulation; syndecan expression;
rowth; FGF-inducible Response Element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetHisLeuAlaLeuProAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                   93WO-FI000514.
94US-00206186.
                                                  9908-00336757
                                                                                                                                         /bound_moiety= "FGF-2 independent nuclear factor"
/note="DNA binding motif 2"
,526. .1551
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1150. .1499
                                                                                                                                                                                            bound_moiety= "FGF-2 dependent nuclear factor"
note="DNA binding motif 3"
                                                                                                                                                                                     497.
                                                                                                                                                                                                                                   bound_moiety= "FGF-2 dependent
note= "DNA binding motif 4"
                                                                                                                                                                                                                                                                                                                    standard name= "Enhancer"
note= "Specifically claimed
                                                                                                                                                                                                                                                                           bound_moiety= "FGF-2 dependent
note= "DNA binding motif 5"
                                                                                                                                                                                                                                                                                                                                                           standard_name= "Enhancer"
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37.00
100.00%
87.50%
84.09%
                                                                                                                                                                                   .1511
                                                                                                                                                                                                                                                                                                          .1446
                                                                                                            _moiety= "FGF-2 independent nuclear factor"
"DNA binding motif 1"
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                                                                                                                                                                                                                                               nuclear factor"
                                                                                                                                                                                                                                                                                       nuclear factor"
                                                                                                                                                                                                                                                                                                                     claim
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Vihinen

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of promoting cutaneous wound healing which comprises directly introducing to a cutaneous wound site a recombinant expression vector comprising the syndecan enhancer element, represents the seponse Element (FiRE), operably linked to a FIRE-activated promoter which is operably linked to a structural gene encoding a growth factor that promotes the cutaneous wound healing. The method is a growthing regeneration of tissue e.g. promotion of hair growth. The invention enhances syndecan expression via administration of growth invention. The enhancer element regulates the expression of syndecan. The factors. The enhancer element regulates the expression of syndecan. The present sequence represents the mouse syndecan enhancer element, FGF-inducible Response Element (FiRE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Promotion of cutaneous wound healing comprises introducing to wound site recombinant expression vector comprising syndecan enhancer element linked to promoter which is linked to structural gene encoding growth factor.
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                                                                                                                                                                                                                                                                                                                                                       Mouse genomic sequence mCG6875
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN45004 standard; DNA; 21562
                                                                                                                                                                                                                                                                                                                             Cytostatic; carcinoma; lymphoma; cancer; murine; gene;
                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-2004
                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                          01-MAR-2002; 2002US-00087192
                                                                 Recombinant nucleic acid useful for diagnosis comprises a nucleotide sequence.
                                                                                                                                                                                                                     28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                               12-SEP-2003
                                                                                                                                                                                                                                                                           WO2003073826-A2.
                                        Claim 1; SEQ ID NO 1735; Opp; English.
                                                                                                            WPI; 2003-328604/31.
                                                                                                                                                                (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1143
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aTGCATGTGGCACTCCCTGCCTCA 1120
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                                                                                            carcinoma
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The present invention relates to novel

DNA and

protein sequences which

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RESULT 15
AAK67239/c
AAK67239;
XX
AAK67239;
XX
O6-NOV-2001 (first entry)
XX
Human immune/haematopoiet:
XX
Human; immune; haematopoiet:
XX
Human immune/haematopoiet:
XX
Homo sapiens.
XX
O9-AUG-2001; 2001WO-US001
XX
17-JAN-2001; 2000US-01906
PR 24-FEB-2000; 2000US-01806
PR 24-FEB-2000; 2000US-01806
PR 16-MAR-2000; 2000US-01806
PR 17-JUN-2000; 2000US-01806
PR 19-MAY-2000; 2000US-01809
PR 11-MAR-2000; 2000US-01809
PR 11-JUL-2000; 2000US-01909
PR 11-JUL-2000; 2000US-02166
PR 28-JUN-2000; 2000US-02166
PR 28-JUN-2000; 2000US-02166
PR 11-JUL-2000; 2000US-02216
PR 11-JUL-2000; 2000US-02216
PR 11-JUL-2000; 2000US-02216
PR 11-AUG-2000; 2000US-02226
PR 11-AUG-2000; 2000US-02226
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Rosen ξ Barash SC, ZS.

2001-483426/52

useful Nucleic cacids encoding human immune/hematopoietic for preventing, diagnosing and/or treating antigen polypeptides, cancers and metastasis.

Disclosure; OI DES ĕ 22051; 3071pp + Sequence Listing; English.

CC AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC concers and treat immune/haematopoietic-related (I), by inserting the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.

Sequence 30393 BP; 8271 A; 7315 Ç 8076 ດ 6731 Ħ, 0 ď 0 Other;

Qy 1 MetHisLeuAlaLeuProAlaSerAla 9	US-10-617-443B-2_COPY_1_9 (1-9) x AAK67239 (1-30393	Alignment Scores: 4.66e+04 Length: 9red. No.: 37.00 Matches: 98.89\$ Conservative: 88.89\$ Mismatches: 77.78\$ Mismatches: 0uery Match: 84.09\$ Gaps: 4
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Minimum DB seq length: 0
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## SUMMARIES

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Best Local Similarity:
                                                                                                         Sequence 654, Application US/09910943
PATENT NO. US20020081610A1
GENERAL INFORMATION:
APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/16148US1
CURRENT APPLICATION NUMBER: US/09/910,943
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 742
                                                               SOPTWARE: PatentIn version 3.1
SEQ ID NO 654
LENGTH: 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/617,443B
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Qi, Jian-shen
APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof FILE REFERENCE: ORT-1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                               ORGANISM: Xenopus laevis
                                                   TYPE: DNA
NAME/KEY: misc_feature
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; OTHER INFORMATION: n may be
US-09-910-943-654
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PRIOR FILING DATE: 2000-03-21
PRIOR PELLOATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELLOATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PELLOATION NUMBER: 60/230,347
PRIOR PELLOATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1 *
SEQ ID NO 13408
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/267,636
PRIOR TILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                TYPE: DNA ORGANISM: Burkholderia fungorum
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Forsyth, R.
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LENGTH: 2157
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CURRENT FILING DATE: 2003-02-20
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PRIOR FILING DATE: 2000-03-21
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FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Burkholderia mallei
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OR FILING DATE: 2000-09-09

REAPPLICATION NUMBER: 60/242,578

OR FILING DATE: 2000-10-23

OR APPLICATION NUMBER: 60/253,625

OR FILING DATE: 2000-11-27

OR APPLICATION NUMBER: 60/257,931

OR APPLICATION NUMBER: 60/257,931

OR APPLICATION DATE: 2000-12-22
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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; APPLICANT: La Rosa, Thomas J.
roplicant: Kovalic, David K.
rhou, Yihua
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TITLE OF INVENTION: Soy Nucleic Acid Molecules
TITLE OF INVENTION: Plants and Uses Thereof fo
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 10035
LENGTH: 1581
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NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 43712
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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CURRENT FILING DATE: 2003-05-14
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ORGANISM: Oryza sativa
FEATURE:
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ORGANISM: Glycine max
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US-10-617-443B-2_COPY_1_9 (1-9) x US-10-424-599-10035 (1-1581)

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RESULT
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APPLICANT: Wang, David G.
TITTE OF INVENTION: Identification and Mapping of Single Nucleotide
TITTE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-2
PRIOR FILING DATE: 2000-03-2
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
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Best Local Similarity:
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SEQ ID NO 88
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APPLICANT: Engelhard, Evic
APPLICANT: Morris, David
TITLE OF INVENTION: NATHONS
FILE REFERENCE: A-71087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 270357, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 241
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LOCATION: (35382)..(35843)
OTHER INFORMATION: "n" at
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NAME/KEY: misc_feature
LOCATION: (5047)...(7943)
OTHER INFORMATION: "n" a
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Matches:
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US-10-617-443B-2_COPY_1_9 (1-9) x US-10-027-632-270357 (1-582)
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DB:
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US-10-027-632-270357/c

US-10-027-632-270357, Application US/10027632

; Sequence 270357, Application US/20030204075A9

; Publication No. US20030204075A9

; GENERAL INFORMATION:
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Best Local Similarity:
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PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-02-24
PRIOR PELLING DATE: 1909-01-23
PRIOR PELLING DATE: 1909-11-23
PRIOR PELLING DATE: 1909-01-23
PRIOR PELLING DATE: 1909-01-23
PRIOR PELLING DATE: 1909-01-23
PRIOR PELLING DATE: 1909-01-23
PRIOR PELLING DATE: 1909-01-28
PRIOR FILING DATE: 1909-01-28
PRIOR FILING DATE: 1909-01-28
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SEQ ID NO 270357
LENGTH: 582
RESULT 11
US-10-437-963-44767
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                                                                                                                                      US-10-617-443B-2_COPY_1_9 (1-9) x US-10-027-632-270357 (1-582)
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Query Match:
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US-10-027-632-270357
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 270357
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10887-1.29
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-09-26
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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                                                                495 CTACACCTGGTACTGCCTGCSTCCGCT 469
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Matches:
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OTHER INFORMATION: n = US-10-087-192-1735
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               Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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SEQ ID NO 1735
LENGTH: 21562
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SEQ ID NO 44767
LENGTH: 4513
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                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MORRIS, DAVIG W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
TITLE OF INVENTION: CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: (1)...(21562)
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                                                                                                                                                                                                                                                TYPE: DNA
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                                                                          . No.:
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Barbazuk, Brad
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                                 Length:
Matches:
Conservative:
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Mismatches:
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                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: US-10-189-099A-5
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Best Local Similarity:
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US-10-322-696-55
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                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-322-696-55
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/189,099A
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 247544
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10189099A
Publication No. US20040005659A1
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Malandro, Marc
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS
FILE REFERENCE: 529452001200
CURRENT APPLICATION NUMBER: US/10/322,696
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 186
                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
FILE REFERENCE: ORT-1644
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Darrow, Andrew L
APPLICANT: Qi, Jian-shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Morris, David W. APPLICANT: Malandro, Marc
                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(247544)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                    LENGTH: 34
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No. US20040166490A1
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Percent Similarity: Best Local Similarity:

Conservative: Mismatches:

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Sequence 5, Application US/10617443B;
Publication No. US20050019777Al

Publication No. US20050019777Al

GENERAL INFORMATION:
APPLICANT: Darrow, Andrew L
APPLICANT: Oi, Jian-shen
APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Chen, Cailin
APPLICANT: Chen, Cailin
Current in Noent Information Number of Series protease and uses thereof
FILE REFERENCE: OGT-1644
FILE REFERENCE: OGT-1644
CURRENT APPLICATION NUMBER: US/10/617,443B
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 34
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-617-443B-5
                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
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Search completed: June 30, 2005, 01:51:25 Job time : 52.1808 secs
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Result
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-QQ/cgn2_1/USPTO_spool/US10617443/runat_29062005_135932_26096/app_query.fasta_1.718
-QB-Issued_Patents_NA -QFMT=fastap_-SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=55its -STRATE1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10617443_@CGN 1 1 93 @runat_29062005_135932_26096 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGE_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPDET0 -LONGLOG-FGAPDEXT=0.5 -FGAPDP=6
-FGAPDEXT=7 -YGAPDP=10 -YGAPDEXT=0.5 -DELOP=6 -DELEXT=7
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length: 2000000000
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Match Length
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Fgapop 6.0 , Fgapext
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US-09-949-016-40949
US-09-949-016-40950
US-09-949-016-40951
US-09-949-016-40952
US-09-949-016-107301
US-08-472-217-3
US-08-472-217-3
US-08-472-217-3
US-08-760-534A-3
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-09-270-767-1 -09-865-879-1 -09-620-312D- -09-620-312D- -08-965-729A-	US-09-949-016-145816 US-09-949-016-146084 US-09-949-016-146352 US-09-949-016-160820 US-09-949-016-160821 US-09-949-016-162623 US-08-340-539A-3 US-08-340-539A-3	-08-467-344A-390 -08-467-344A-390 -08-424-550B-390 -08-424-550B-393 -09-949-016-15660 -09-949-016-15662 -09-949-016-15663 -09-949-016-15663 -09-949-016-76709	-09-949-016-129 -09-949-016-124 -09-620-3120-783 -09-629-902-540-783 -08-639-857-32 -08-469-260A-39 -08-488-446-393
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## ALIGNMENTS

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Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION
APPLICANT: FIREISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DUA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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                                                    US-10-617-443B-2_COPY_1_9 (1-9) x US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1
                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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1987705 GTTCACTTAGCGATGCCGGCGTCAGCT 1987679

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FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 40948
                                                                                        Score:
                                                                                                                                                                        US-09-949-016-40949
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 40949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40949, Application US/09949016 Patent No. 6812339
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                               LENGTH: 601
TYPE: DNA
                                                                                                                                                                                                ORGANISM: Human
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84.09%
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Alignment Scores:
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Best Local Similarity:
Query Match:
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; ORGANISM: Human
US-09-949-016-40950
                                                                                   ; ORGANISM: Human
US-09-949-016-40951
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                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISSASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,488
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/331,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 40950
LENGTH: 601
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Patent No. 6812339
                                                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40951, Ap
Patent No. 6812339
                                                                                                                             TYPE: DNA
                                                                                                                                                 2 ID NO 40951
SENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-40952
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DB:
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Best Local Similarity:
Query Match:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40952
                                    SEQ ID NO 107301
LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                    Sequence 107301, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                         CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                       .09-949-016-107301
                                                                                                                      PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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PRIOR FILING DATE: 2000-09-08
                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                  RIFILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED RIFILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equence 40952, Application US/09949016
atent No. 6812339
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ORGANISM: Human
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OF DETECTION AND USES
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                          TELEPHONE: (202) 371-26
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/OCKET NUMBER: 33,851
REFERENCE/OCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2196 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele 22 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US OF FILING DATE: 07-MAR-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US OF APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
MOLECULE TYPE:
HYPOTHETICAL:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                               STRANDEDNESS:
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                                                                                                                                              TYPE: nucleic acid
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                                                                                 COPOLOGY:
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                                                                                                                                                                                     2196 base pairs
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Mali, Markku
Vihinen, Tapani
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                                      DNA (genomic)
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Indels:
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Matches:
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Alignment Scores:

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RESULT 9
US-08-760-534A-3/c
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Best Local Similarity:
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                                           US-10-617-443B-2_COPY_1_9 (1-9) x US-08-760-534A-3 (1-2196)
                                                                                                Best Local Similarity:
Query Match:
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                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                               NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE LOCKET NUMBER: 1708
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2640
TELEPHONE: (202) 371-2640
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
IENCENT: 216 has being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 3, Application US/08760534A Patent No. 6017727
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/760,534A
FILING DATE: 02-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/206,186
FILING DATE: 07-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/F193/00514
FILING DATE: 01-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                   LENGTH: 2196 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
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                 MetHisLeuAlaLeuProAlaSer 8
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1100 NEW YORK AVENUE, SUITE 600
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Conservative:
Mismatches:
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Gaps:
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US-09-336-757-3/c
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Query Match:
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                                                                                                                                                                                                  US-10-617-443B-2_COPY_1_9 (1-9) x US-09-336-757-3
                                                                                   US-09-949-016-16873
                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                      Percent Similarity:
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Patent No. 6492344
Sequence 16873, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
foliation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/336,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: JALKANEN, MARKKI
APPLICANT: JAKKOLA, PANU
APPLICANT: VIHINEN, TAPANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SYNDECAN ENHANCER ELEMENT AND SYNDECAN TITLE OF INVENTION: STIMULATION OF CELLULAR DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 01-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CIMBALA, MICHELE P
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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Matches:
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; LENGTH: 150780
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14711
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16873
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RESULT 13
US-09-949-016-12900/c
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 14711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 20/022
SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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atent No. 6812339
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Query Match:
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US-10-617-443B-2_COPY_1_9 (1-9) x US-09-949-016-12412 (1-476044)
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                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIV
                                                                                                                                                                                                                                                                                                                          SOFTWARE: Fast
SEQ ID NO 12412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12412, Application US/09949016 Patent No. 6812339
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Human
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Matches:
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1 MetHisLeuAlaLeuProAlaSer 8

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RESULT 15

US-09-620-312D-992/c

Sequence 992, Application US/09620312D

Patent No. 6569662

PATENT TO SEGGE 2

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Zhao, Qing A.

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Webrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Jian-Rui
APPLICANT: Yang, Jian-Rui
APPLICANT: Ang, Jian-Rui
APPLICANT: Mang, Jian-Rui
APPLICANT: Mang, Jian-Rui
APPLICANT: Mang, Dinrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
ITILE OF INVENTION: No. 6569662el Nucleic Acids and
ITILE OF INVENTION: Polypeptides
FILE REFERENCE: 786172B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 992
LENGTH: 1854
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1854)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-992
                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: June 30, 2005, 01:41:07 Job time : 496.029 Becs
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                                                                                                                                                               US-10-617-443B-2_COPY_1_9 (1-9) x US-09-620-312D-992 (1-1854)
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Pred. No.:
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NAME/KEY: CDS
LOCATION: (559)..(1710)
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Matches:
Conservative:
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Result
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-Q=/cgn2_1/USPTO_spool/US10617443/runat_29062005_135932_26076/app_query.fasta_1.718
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-DB=EST -OFMT=fastap -SUPFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10617443 @CGN 1 4385 @runat_29062005_135932_26076 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Ygapop 10.0 , y
Fgapop 6.0 , I
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AV912337
                                         BJ457822
BJ474645
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CD662805
AV912195
CD66262622
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 BJ457822
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                                                                                                                       Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                         Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                       BJ457822 K. Sato unpublished colvegetative stage leaves Hordeum baak29g22 3', mRNA sequence.
                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                          Contact: Tadasu
                                                                                                                                                                                                      Sato, K., Saisho, D. and Takeda, K. Barley EST sequencing project in Unpublished (2002)
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1 (bases 1 to 150)
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/cultivar="Akashinriki"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baak29g22"
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BU4525679

BU452679

BU452679

BU452679

BU452679

BU500006

BE213796

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BJ455746
BJ458684
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NA library, cv. Akashinriki
vulgare subsp. vulgare cDNA clone
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BJ455746
BJ456746
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AJ4347870782
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CB877648
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BJ448746
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AJ451181
HO15D118
AJ25121
HP0502
10h1
HP060127
WHE0564 F
SC01 10b1
AV490381
AV490381
PH08G1177
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RESULT 2
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Center For Genetic Resource Information National Institute of Genetics 1111 Yates, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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EST.
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Location/Qualifiers
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Akashinriki vegetative stage leaves"
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/dev_stage="adult, heading stage"
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100.00%
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BJ450407 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
baak29g22 5', mRNA sequence.
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermattophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Spermattophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.

1 (bases 1 to 234)
1 (Closes, T.J., Fenton, R.D., Wanamaker, S., Collura, K.,
Wahid, A., Close, T.J., Fenton, R.D., Wing, R. and Yu, Y.
Drought-stressed barley leaf epidermis cDNA sequences
Unpublished (2003)
Contact: Timothy J. Close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato,K., Saisho,D. and Takeda,K. Barley EST sequencing project in Unpublished (2002)
                                                                                                                                                                                                                                                                     CD662805 mRNA linear UCRHV18_03ag11_b1 Drought-stressed Dicktoo barley library Hordeum vulgare subsp. vulgare cDNA clone
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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1 (bases 1 to 202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Štreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ450407.1 GI:21129011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tadasu Shin-i
                                                                                                                                                                                                      EST
                                                                                                                                                                                                                      CD662805
CD662805.1 GI:32153419
                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"
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/cultivar="Akashinriki"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sub_species="vulgare"
/db_xref="taxon:112509"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213
41.00
100.00%
88.89%
93.18%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lone="baak29g22"
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Matches:
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8
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epidermis cDNA
UCRHV18_03ag11,
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Percent Similarity:
Best Local Similarity:
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                                        1 MetHisLeuAlaLeuProAlaSerAla 9
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University of California
Riverside, CA 92521-0124, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 909-787-4437
CTTCATTTGGCGCCTGCCGGCGTCGGCT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indicative vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Seeds of barley (Hordeum vulgare L. cv. DickToo) were germinated in dishpans containing UCR-mix soil. Seedlings were kept in a growth chamber at 20C (day/night) and allowed to grow at 60-70% soil moisture content. After 3-4 days, the water was withheld in order to apply drought until the soil moisture content was reduced to 10-12%, which took another 3-4 days. At the time of extraction of epidermis, leaf water and osmotic potentials and extracted lower epidermis osmotic potentials had dropped to 15.9%, 20.2% and 24.7% of controls, respectively, as determined using a vapor pressure osmometer (Model 5100C, Wescor, Inc., Logan, UT). Epidermal strips were quickly peeled off of seedlings and immediately submerged in liquid nitrogen. About 15-20 g of epidermal tissue was collected and used to extract total RNA. Total RNA was extracted using Concert plant RNA Reagent (Invitrogen 12322-012). Poly(A) RNA was purified using bolyATTack mRNA Isolation System IV (Promega). A cDNA library was made using a Uni-ZAP cDNA synthesis kit (Stratagene). A total of 1 million primary lambda cDNA clones were mass-excised in vivo to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Plasmid DNA purified, cDNA clones archived, and DNA sequences determined using the TJ primer (mainly 3' end reads) using an AB13730 at the Arizona Genomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          timothy.close@ucr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at Riverside (by Wanamaker) using the HarvEST pipeline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to high quality region. Sequences that retained a nhred 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute, University of Arizona (Collura, Feuerbacher,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="1-2 week seedlings"
/lab_host="E. coli TJC121"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uality region. Sequences that retained a phred 17 of at least 100 bases were deposited to GenBank."
                                                                                                                                 CD662805 (1-234)
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Matches:
Conservative:
Mismatches:
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RESULT 6
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AUTHORS
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AUTHORS
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AV912195
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KEYWORDS:
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CD662622.1
EST.
                 Pooideae; Triticeae; Hordeum.

1 (Dases 1 to 314)
Wahid,A.; Close,T.J., Fenton,R.D., Wanamaker,S.; Collura,K.,
Feuerbacher,O., Kim,H.R., Kudrna,D., Wing,R. and Yu,Y.
Drought-stressed barley leaf epidermis cDNA sequences
Unpublished (2003)
                                                                                                                    Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetHisLeuAlaLeuProAlaSerAla 9
                                                                                                                                                                                                                                                                                                        CD662622 314 bp mRNA linear EST 23-JUN-20
UCRHV18_02cc08_b1 Drought-stressed Dicktoo barley epidermis cDNA
library Hordeum vulgare subsp. vulgare cDNA clone UCRHV18_02cc08
                                                                                                                                                                                                                                                                                             mRNA sequence.
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Tel: 81-559-81-6856
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1 (bases 1 to 308)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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AV912195 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDN
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Location/Qualifiers
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Timothy J. Close
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/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"
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/db_xref="taxon:112509"
/clone="baak1f21"
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/cultivar="Akashinriki"
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Matches:
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                                                                                             US-10-617-443B-2_COPY_1_9 (1-9) x CD662622 (1-314)
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Best Local Similarity:
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                                                1 MetHisLeuAlaLeuProAlaSerAla 9
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University of California
Riverside, CA 92521-0124, USA
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Fax: 909-787-4437
                                                                                                                                                                                                                                                                                                                                                                                                Inter Yector: Lambda Uni-ZAP XR, excised phagemid; Site 1: ECORI; Site 2: XhOI; Seeds of barley (Hordeum vulgare L. cv. DickToo) were germinated in dishpans containing UCR-mix soil. Seedlings were kept in a growth chamber at 20C (day/night) and allowed to grow at 60-70% soil moisture content. After 3-4 days, the water was withheld in order to apply drought until the soil moisture content was reduced to 10-12%, which took another 3-4 days. At the time of extraction of epidermis, leaf water and osmotic potentials and extracted lower epidermis of controls, respectively, as determined using a vapor pressure osmometer (Model 5100C, Wescor, Inc., Logan, UT). Epidermal tissue was collected and used to extract total needlately submerged in liquid nitrogen. About 15-20 g of epidermal tissue was collected using Concert plant RNA Reagent (Invitrogen 1232-012). Poly(A) RNA was purified using PolyATrack mRNA Isolation System IV (Promega). A cDNA library was made using a Uni-ZAP cDNA synthesis kit (Stratagene). A total of 1 million primary lambda cDNA clones were mass-excised in vivo to give a population of performed in the TJ Close lab at the University of California, Riverside by A. Wahid with some assistance from R.D. Fenton. Phagemids were plated on the TJC121 host strain, plasmid DNA purified, cDNA clones archived, and DNA sequences determined using the TJ primer (mainly 3' end reads) using an ABIJ730 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Contagined to GenBank "
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/lab_host="E. coli TJC121"
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tissue_type="lower leaf epidermis"
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/cultivar="Dicktoo"
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41.00
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Indels:
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Matches:
Conservative:
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                     REFERENCE
AUTHORS
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US-10-617-443B-2_COPY_1_9 (1-9) x AV909564 (1-329)
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                                                                                                            Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (Dases 1 to 332)
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AV909564 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
                      Unpublished (2002)
Contact: Tadasu Shin-i
                                                                 Sato, K., Saisho, D. and Takeda, K. Barley EST sequencing project in
                                                                                                                                                                                                                                                                                          AV911456.1 GI:18207233
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Contact: Tadasu Shin-i
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poacese;
Center For Genetic Resource Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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/clome_lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
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/cultivar="Akashinriki"
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RESULT 9
AV912337
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Best Local Similarity:
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AV912337
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Barley EST sequencing project in NIG and Okayama Univ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare subsp. vulgare
                                                                                                                                                                                                                                     Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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1 (bases 1 to 419)
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Location/Qualifiers
          /sub_species="vulgare"
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/tissue_type="leaves"
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Akashinriki vegetative stage leaves"
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/dev_stage="vegetative_stage"
/clome_lib="K. Sato unpublished_cDNA_library,
Akashinriki vegetative_stage-leaves"
                                                                                                                                                    /mol_type="mRNA"
/cultivar="Akashinriki"
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/db_xref="taxon:112509"
/clone="baak13e01"
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Matches:
Conservative:
Mismatches:
Indels:
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NA library, cv. Akashinriki
vulgare subsp. vulgare cDNA clone
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Alignment Scores:

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RESULT 11
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AV910159/c
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   ACCESSION
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BJ461882 A40 bp mRNA BJ461882 K. Sato unpublished cDNA library, vegetative stage leaves Hordeum vulgare sul baak21b12 3', mRNA sequence.
BJ461882
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                                                                                                                                        Sato,K., Saisho,D. and Takeda,K. Barley EST sequencing project in Unpublished (2002)
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 81-559-81-6856 Fax: 81-559-81-6855
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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1 (bases 1 to 427)
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Akashinriki vegetative stage leaves"
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/db_xref="taxon:112509"
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                               subsp. vulgare cDNA clone
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Akashinriki
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BJ455746
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AUTHORS
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JOURNAL
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VERSION
KEYWORDS
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M Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embr
Spermatophyta; Magnollophyta; Liliopsida; Po
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 440)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okar
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EST.
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Location/Qualifiers
                                                                                                                 Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 446)
1 (bases 1 to 446)
1 Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                              446 bp mRNA linear EST 23-WAY-20 BJ455746 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baakl8a21 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetHisLeuAlaLeuProAlaSerAla 9
                                  Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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BJ455746.1 GI:21134312
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Location/Qualifiers
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a; Poales; Poaceae;
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BJ458684
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BJ458684
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Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 469)
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Contact: Tadasu Shin-i
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BJ458684.1 GI:21137220
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Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                           Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Akashinriki vegetative stage leaves"
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US-10-617-443B-2_COPY_1_9 (1-9) x BJ458684 (1-469)

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BJ448746/c
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                BJ447999 487 bp mRNA linear EST 23-MAY-200
BJ447999 K. Sato unpublished cDNA library, cv. Akashinriki
vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
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BJ448746 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak21b12 5', mRNA sequence.
BJ448746
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BJ447999.1 GI:21126629
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 482)
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Location/Qualifiers
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Akashinriki
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Search completed: June 30, Job time : 161.519 secs

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                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                           source
 343
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Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
                          1 MetHisLeuAlaLeuProAlaSerAla 9
                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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CTTCATTTGGCGCTGCCGGCGTCGGCT 317
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41.00
100.00%
88.89%
93.18%
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                                                               (1-9) x BJ447999 (1-487)
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Matches:
Conservative:
Mismatches:
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Result
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Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                      Score
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Copyright (c) 1993 - 2005 Compugen Ltd.
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## ALIGNMENTS

ORIGIN	JOURNAL FEATURES SOURCE	ORGANISM REFERENCE AUTHORS	RESULT 1 AX338509 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE
/organism="Homo sepiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" /note="Incyte ID No: 7474343CB1"	Patent: Wi Incyte Ge		AX338509 1797 bp DNA linear PAT 09-JAN-2002 Sequence 28 from Patent WO0183775. AX338509 AX338509.1 GI:18128931

Alignment Scores:

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GAGTCTCCTCCTACTGGAGGTGCGGCGGGGAACGACCTCCTCTTCAGCATCGCA
        GluSerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAla 329
                                                                                     GlnGluValAlaProAsnSerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIle
                                                                                                              GTGGATGAGCTGAAGGCCAGCAACCCGGACTTCCCCAGAGGTCAGCAGTGGAATTTATGTG
                                                                                                                        ValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrVal
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PC A61P
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Matrix-remodeling genes

Patent: JP 2002527054 A 14 27-AUG-2002;

INCYTE PHARMACEUTICALS INC

OS Homo sapiens (human)

PAUG-2002

PAUG-2014

PD 27-AUG-2002

PD 207-E199 JP 2000575891

PF 06-CCT-1998 US 09/169289

PI MICHAEL G WALKER, WAYNE VOLKMUTH, TOD M KLINGLER PC
C12N15/09, A61K38/00, A61K38/28, A61K38/46, A61K48/00, A61P1/04,

A61P3/10
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A61K37/54
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/db_xref="taxon:9606"
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Homo sapiens pregnancy-related &
cds; alternatively spliced.
AY280665
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                  1 (bases 1 to 2543)
Nie,G.Y., Hampton,A., Li,Y., Findlay,J.K. and Salamonsen,L.A.
Nie,G.Y., Hampton,A., Li,Y., Findlay,J.K. and Salamonsen,L.A.
Identification and cloning of two isoforms of human
high-temperature requirement factor A3 (HtrA3), characterization
tits genomic structure and comparison of its tissue distribution
with HtrA1 and HtrA2
Biochem J. 371 (Pt 1), 39-48 (2003)
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Nie,G., Hampton,A., Li,Y., Findlay,J.K. and Direct Submission
Submitted (22-APR-2003) Prince Henry's Insti
Research, 246 Clayton Rd., Melbourne, Victor
Location/Qualifiers
                                                        ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp
                                                                                                                                                                                                                                                                                                                                                                                                            AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr
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 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro
                                                                                                                              AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr
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                                    GTGACAACGGCATCGTCAGCACTGCCCAGCGGAGGGCAGGGAAGCTGGGCCTCCGGGAC
                                                                                                        GACCTGCGGCCTGGGGAGTTTGTGGTGGCCATCGGCAGTCCCTTCGCCCTACAGAACACA
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/brotein_id="AAP42282.1"
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LRHPLFGRNVPLSGSGFTVNGLGVSAAPGRQQLXVQLOMGDSYBAT
IKDIDKKSDIATIKIHPKKKLPVLLLGHSADLRPGEFVVAIGSPFALQNTVTTGIVST
AQBEGRELGLRDSDMDYIQTDAIINYGNSGGPLVNLDGEVIGINTLKVTAGISFALPS
DRITRFLTEEQDKQIKDWKKRFIGIRMRTITPSLVDELKASNPDFPEVSSGIYVQEVA
PNSPSQRGGIQDGDIIVKYNGRPLVDSSELQBAVLTESPLLLEVRRGNDDLLFSIAPE
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/chromosome="4"
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                                                                                                                                                                                                                                                                                                          Submitted (05-JUN-2002) Proteome Discovery, Oxford Glycosciences, The Forum, 86 Milton Park, Abingdon, Oxon OX14 4RY, UK Sequence update by submitter on Jun 5, 2002 this sequence version replaced gi:14700055.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2554)
Southan, C. and Punia, P.K.
Direct Submission
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AY040094
Homo sapiens serine protease
AY040094
AY040094.2 GI:21326482
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Southan, C
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222 1583
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                                                                     1326 GTGGATGAGCTGAAGGCCAGCAACCC
                          270
                     GlnGluValAlaProAsnSerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIle 289
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VVM"

665

29

69 725 49

1. Roces:	26 GTGGATGAGGCCAGCCAGCCCGGACTTCCCAGAGGTCAGCAGTGGAATTTI	<b>3</b>
nment Scores: 1.67e-130 Length: 2554 2. No.: 1635.00 Matches: 2554 25cnt Similarity: 100.00% Mismatches: 25c	250 ValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTy	Ś
mment Scores:  1.67e-130    Iength: 2554   1635.00   Matches: 0   Matc	.266 ATCAAAGACTGGAAGAAGCGCTTCATCGGCATACGGATGCGGACGATCACACCAAG	망
mment Scores:  1.67e-130  1.635.00  Matches: 2554  26c	30	Qy
mment Scores:  1.67e-130  1.80::  1.635.00  Matches:  2554  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  250:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:  260:	206 TCCTTTGCCATCCCCTCAGACCGCATCACACGGTTCCTCACAGAGTTCCAAGACAAG	문
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1.67e-130   Length:   2554     1. No.:   1635.00   Matches:   325     2. Cent Similarity:   100.00%   Mismatches:   0     1. Local Similarity:   100.00%   Mismatches:   0     1. Local Similarity:   100.00%   Mismatches:   0     1. Local Similarity:   97.38%   Indels:   0     1. Local Similarity:   100.00%   Indels:   100.00%   Inde	86 AATGCCCACGTGGTGTCCAG	В
### Property   1.67e-130   Length:   2554	0 AsnAlaHisValValSerSe	ş
### Property   1.67e-130   Length:   2554	26 AACGTGCCCCTGTCCAGCGG	Дb
1.67e-130   Length:   2554     1. No.:   1635.00   Matches:   325     1. cel   100.00%   Mismatches:   0     1. cel   Similarity:   100.00%   Mismatches:   0     1. cel   Similarity:   100.00%   Mismatches:   0     1. cel   Similarity:   97.38%   Indels:   0     1. cel   Similarity:   97.38%   Gaps:   0     1. cel   Similarity:   0   0   0   0     1. cel   Similarity:   0   0   0   0     1. cel   Similarity:	0 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleI]	Ş
1.67e-130   Length:   2554     1.00:   1635.00   Matches:   325     2.00:   1635.00   Matches:   325     2.00:   100.00%   Mismatches:   0     2.00:   100.00%   Indels:   0     2.00:   2.00%   Indels:   0     3.00:   2.00%   Indels:   0     3.00:   2.00%   Indels:   0     3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.00:   3.0	66 AAGATCGCACCAGCCGTGGTCCACATAGAGCTCTTCCTGAGAC	탕
### Park Scores: 1.67e-130 Length: 2554  1. No.: 1635.00 Matches: 325    Cont Similarity: 100.00% Mismatches: 0	0 LysileAlaProAlaValValHisileGluLeuPheLeuArgH	8
1.67e-130   Length: 2554     1. No.:   1635.00   Matches: 325     2. ce:   100.00%   Conservative: 0     3. colored Similarity:   100.00%   Mismatches: 0     4. colored Similarity:   100.00%   Mismatches: 0     5. colored Local Similarity:   100.00%   Indels: 0     6. colored Local Similarity:   100.00%   Indels: 0     7. dels:   9.38%   Gaps: 0     10.617-443B-2 (1-334)	06 GGTCTCCACCAGCTGAGCAGCCCGCGCTACAAGTTCAACTTCATTGCTG	망
gnment Scores:     1.67e-130     Length:     2554       1. No.:     1635.00     Matches:     325       re:     1635.00     Matches:     0       cent Similarity:     100.00%     Conservative:     0       t Local Similarity:     100.00%     Mismatches:     0       ry Match:     9     7.38%     Indels:     0       gaps:     0     0       10-617-443B-2 (1-334)     x AY040094 (1-2554)	0 GlyLeuHisGlnLeuSerSerProArgTyrLysPheAsnPheIleAlaA	Ş
gnment Scores:     1.67e-130     Length:     255       i. No.:     1635.00     Matches:     325       re:     100.00%     Conservative:     0       cent Similarity:     100.00%     Mismatches:     0       t Local Similarity:     100.00%     Mismatches:     0       y7.38%     Indels:     0       Gaps:     0	-443B-2 (1-334) x AY040094 (1-2554)	10-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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McKernan, M.J., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
P. 1247932
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     Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Kowis, C.R., Sneed, A.J., Martin, R.G., Muz
A.N., Gibbs, R.A.
                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
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Submitted (02-JUL-2002) National Institutes of Health, Mammalian Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Homo sapiens serine protease HTRA3,
IMAGE:5180585), complete cds
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Tissue Procurement: Life Technologies, Inc.
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Clone distribution: MGC clone

distribution information can be found

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AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr 149

AlaThrIleLysIleHisProLysLysLysLeuProValLeuLeuLeuGlyHisSerAla

GCCACCATCAAGATCCATCCCAAGAAAAAGCTCCCTGTGTTGTTGCTGGGTCACTCGGCC

948 129

GÁCCTGCGGCCTGGGGAGTTTGTGGTGGCCATCGGCAGTCCCTTCGCCCTACAGAACACA

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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-617-443B-2 (1-334) x BC034390 (1-2585)
829
                                                                                                                                                                                                                                                                                             649
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This clone was selected for full length sequencing because
passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                            LeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIleAspLysSerAspIle
                                                                                                                                                                                                                                AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr
                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLeuHisGlnLeuSerSerProArgTyrLysPheAsnPheIleAlaAspValValGlu
                                                                                                AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGln
                                                                                                                                                                                               AAGATCGCACCAGCCGTGGTCCACATAGAGCTCTTCCTGAGACACCCGCTGTTTGGCCGC
                                                                                                                                                                                                                                                                                                                                           LysIleAlaProAlaValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArg
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LQAASRRALOLSGTPVRQLOXGACPLOSPCGESLECVRGLCRCRWSHAVCHILE
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QREGRELGLROSDMVJCOTDAIINYGNSGGPLVNLDGEVASNPDFPEVSSGIYVQEVA
DRITRFLTEFQDKQIKDMKKRFIGIRMRTITPSLVDELKASNPDFPEVSSGIYVQEVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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Indels:
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888
                                                109
                                                                                                828
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                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                708
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RESULT 6
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VERSION
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Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Sklausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Bouffard, S., Kraywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2586)

1 (bases 1 to 2586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE:5588608), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProGluValValMet 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGACAACGGGCATCGTCAGCACTGCCCAGCGGGAGGGCAGGGAGCTGGGCCTCCGGGAC 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTCTCCTCCTACTGGAGGTGCGGCGGGGGAACGACCTCCTCTTCAGCATCGCA 1548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCAAGGTCAACGGGCGTCCTAGTGGACTCGAGTGAGCTGCAGGAGGCCGTGCTGACC 1488
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9 MGC:46243
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Query Match: DB:

Percent Similarity: Best Local Similarity:

1.69e-130 1635.00 100.00% 100.00% 97.38%

Length:
Matches:
Conservative:
Mismatches:
Indels:

2586 0 0 0

Score: Alignment

Pred. No.:

Scores:

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REMARK
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PUBMED
REFERENCE
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 79 Row: e Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24475740. Location/Qualifiers
1. .2586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web Bite: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgrl.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi.P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
McDowell,J., Mastello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Invitrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Ovary, pooled from 3 adults"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lone="MGC:46243 IMAGE:5588608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _xref="LocusID:94031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 2586
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Nie,G., Li,Y., Findlay,J.K. and
Identification and cloning of a
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                                                              Sakamoto,T. and Takeda,S.
BIC-interacting proteins and use thereof
Patent: WO 2004083241-A 40 30-SEP-2004;
Takeda Chemical Industries, Ltd. (JP)
Location/Qualifiers
                                                                                                                     Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Sequence 40 from Patent
CQ879976
CQ879976.1 GI:54033832
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ATCCCTGAGGTGGTCATG 150:
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                                                                                                                                                                                    1338 bp DN
Patent WO2004083241.
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             AACGAGTCTTCACTCCTGCTGGAGGTGCGGCGAGGCAATGATGATCTCCTCTTCAGCATC
                        ThrGluSerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIle
                                                ATCGTCAAAGTCAATGGCCGCCCCCTGGCGGATTCCAGCGAGCTGCAGGAGGCAGTCCTG
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Tsurumai-cho, Nagoya, Aichi 466-8550,
Location/Qualifiers
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Unpublished
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           ArgAsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIle
                                                  GluLysIleAlaProAlaValValHisIleGluLeuPheLeuArgHisProLeuPheGly
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/product="coll-associated Berine protease"
/protein_id="AAK70226.1"
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/db_xref="col:14626471"
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DAYEATIQDIDKKSDIATIVIHPKKKLPVLLLGHSADLRPGEFVVAIESPLCPAEHRD
KCIVSTAQRTGKELGLADSDMDYIGTDAIINGKSGFPLVALDGEVIGINTLKVAAGI
SFAIPSDRITRFLSEFQNKHVKDWKKRFIGIRMRTITPSLVEELKAANPDFPAVSSGI
YVQEVVPNSPSQRGGIQDGDIIVKVNGRFPLADSSELQBAVLNESSILAAEVRRGNDDL
LFSIIPEVVM"
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/note="TASP"
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strain="BALB/c"
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Boardman, P.E., Bonfield, J.K., Brown, W.R.A., Carder, C., Cha Croning, M.D.R., Davies, R.M., Francis, M.D., Grafham, D.V., Hubbard, S.J., Humphray, S.J., Hunt, P.J., Maddison, M., McLar Niblett, D., Overton, I.M., Rogers, J., Scott, C.E., Taylor, R.
                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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Boardman, P.E., Bonfield, J.K.,
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Direct Submission
Submitted (09-MAR-2004) Sanger Institute, Hinxton, Cam
Submitted (09-MAR-2004) Sanger Institute, Hinxton, Cam
CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosth. cDNA was prepared from RNA extracted from small intestine, normalised, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B.
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This sequence is from the
                GlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAspGly
                                                     PheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIleVal
                                                                                                                                                                       ProLysLysLysLeuProValLeuLeuGlyHisSerAlaAspLeuArgProGlyGlu
                                                                                                                                                                                                             TATGAAGCAACCATCAGAGACATTGACAAGAAATCTGACATTGCAACAATAAAGATCCAC
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    CAGACAGATGCTATTATCAATTATGGCAACTCTGGAGGACCTCTAGTTAATCTGGATGGT
                                                                       SerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrIle
                                                                                                        TTTGTAGTGGCAATTGGAAGCCCATTTGCCCCTACAGAACACTGTGACAACAGGTATTGTC
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/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="Ch8ST625h5"
/clone_lib="CSEQCHN56"
/dev_stage="adult"
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Gallus gallus finished cDNA,
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Submitted (02-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. B-mail enquiries: chickest@bms.umist.ac.uk
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1. (bases 1 to 2176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus
                                                                                                                                                                                                                                                                                                                                    BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, 
from a library constructed by Elizabeth Bosch. cDNA was prepared 
from RNA extracted from limbs, normalised, and poly A-trimmed. 
ECORI-NOtI cut cDNA was then ligated into the vector. Vector: 
pBluescript II KS(+); Site_1: ECORI; Site_2: NotI Host: Eschericl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX929862.1
                                                                                                                                                                                                                                                                                                                     pBluescript II KS(+); Site_1: coli DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing project.
This sequence is from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tickle, C. and Wilson, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTGATTGGAATTAACACCTTGAAGGTTACAGCTGGAATTTCCTTTGCTATTCCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIleProSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATAATGCTGATTTTCCTGATGTCAGGAGTGGAATTTACGTACATGAAGTTGTTCCAAAT 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerAsnProAspPheProGluValSerSerGlyIleTyrValGlnGluValAlaProAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTTTCATTGGCATCCGAATGCTGACAATAACACCTGCCTTGGTGGAAGAATTGAAACAC 954
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                                                                                                                                                                                                    /organism="Gallus gallu
/mol_type="mRNA"
/strain="White Leghorn,
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                    /clone="ChEST656k24"
/clone_lib="CSEQCHN38"
                                                                                                                                                                            /db_xref="taxon:9031"
                                                                                                         dev_stage="stage"
9.23e-115
1450.50
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  Length:
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GluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaProGluValValMet
                                           CCTTTGATGACTTCCAGTGACCTTCAAGAGGCTGTGATGAACGAATCACCTCTACTACTT
                                                                                                                                                                                                                         ArgPheIleGlyIleArgMetArgThrIleThrProSerLeuValAspGluLeuLysAla 255
                                                                                                                                                                                                                                                                              AspArgIleThrArgPheLeuThrGluPheGlnAspLysGlnIleLysAspTrpLysLys
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                                                                                                                                                   AATAATGCTGATTTTCCTGATGTCAGGAGTGGAATTTACGTACATGAAGTTGTTCCAAAT
                                                                                                                                                                    GAAGTGATTGGAATTAACACCTTGAAGGTTACAGCTGGAATTTCCTTTTGCTATTCCGTCG
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                                                           ProLeuValAspSerSerGluLeuGlnGluAlaValLeuThrGluSerProLeuLeuLeu
                                                                                                                         SerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArg
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                                                                                                                                                                                                        CGTTTCATTGGCATCCGAATGCTGACAATAACACCTGCCTTGGTGGAAGAATTGAAACAC
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FEATURES

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 178 Row: 1 Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Clone distribution:

MGC clone distribution

information can be found

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Location/Qualifiers
1. .2080

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PUBMED
REFERENCE
AUTHORS
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Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetcw, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,

McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,

Schnerch, A., Schain, J. E., Jones, S. J. and Marra, M. A.

Generation and initial analysis of more than 15,000 full-length

human and mouse CDNA sequences
                     Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard;G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: National Institutes of Health In Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-JUL-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                          Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Director MGC Project.
Direct Submission
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1 (bases 1 to 2080)
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/clone="MGC:91963 TMAGE:7041654"
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1 (bases 1 to 1953)

Nie,G.Y., Hampton,A., Li,Y., Findlay,J.K. and Salamonsen,L.A.

Identification and cloning of two isoforms of human high-temperature requirement factor A3 (HtrA3), characterization of the genomic structure and comparison of its tissue distribution with HtrA1 and HtrA2

Biochem. J. 371 (Pt 1), 39-48 (2003)

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                                                                                                                                                                                                 Nie, G., Hampton, A., Li, Y., Findlay, J.K. and Salamonsen, L.A. Direct Submission
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Conservative: Mismatches: Indels: Gaps:

Length: Matches:

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US-10-617-443B-2 (1-334) x AY280666 (1-1953)

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                                                       SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro
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/mol_type="unassigned
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Nie,G., Li,Y., Findlay,J.K. and Salamonsen,L.A. Identification and Cloning of a novel pregnancy-related
                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-APR-2003) Prince Henry's Institute of Medical Research, 246 Clayton Rd, Melbourne, Victoria 3168, Australi Location/Qualifiers
1. .1897
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                                 /codon_start=1
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YHIELFURHPLFGRNVPLSSGSGFIMSEAGLIVTNAHVVSSSSTASGRQDLKVQLQNTVT
DAYEATIQDIDKKSDLATIVIHPKKLPVLLGHSADLRPGEFVVAIGSPFALQNTVT
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/note="alternatively spliced"
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Result
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-Q=/cgn2 1/USPTO spool/US10617443/runat 29062005 135931 26052/app query.fasta_1.718
-Q=/cgn2 1/USPTO spool/US10617443/runat 29062005 135931 26052/app query.fasta_1.718
-DB=N Gemeseq 16Dec04 -QFWT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0.
-LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -WATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USEX=US10617443 @CGN 1 1 586 @runat 29062005 135931 26052 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Adj11355 Human PRS
Aad44189 Mouse TAN
Ado01101 Human ser
Ado01102 Human ser
Ado01091 Human ser
                                                                                                                                                          Description
     RESULT 1
ADJ11355
ID ADJ1355
AC ADJ1
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Acn89676 Breast ca	ACN89676	11	2437	61.6	34.5
CDNA	AAT75444	ง	o o	61.6	4. 4
Adl13863 Osteoarth	ADL13863	10	95	61.6	34.5
	ADJ56226	10	8	•	4
~	ADL13867	10	င္မ	•	4
6 Human e	ADR40166	13	2036	61.6	34.5
4 Breast	ADR24954	Ľ	င္မ		4
	ABV78051	σ	2036		4
×	ADS73135	7	2034	61.6	4.
9	ADS10059	13	1973	•	4
_	ADB62641	10	1894	•	4.
Adll3865 Osteoarth	ADL13865	10	1443	•	٠.
4	ADL13864	10	1443	•	34.5
	AAZ29176	w	1443	61.6	34.5
	AAD44188	σ	1440	•	34.5
CDNA	AAZ29195	ω	1185	61.6	34.5
Full 1	ACF12815	œ	1897	63.0	1057
Humar	AAS26848	4	1788	٠	1105
Human	ACF12811	œ	1953	66.5	1117
Aas14885 Human cDN	AAS14885	4.	1695	•	1122
0	ADO01100	12	1075	•	1144
. Aas26920 Human cDN	AAS26920	4.	1868	82.1	1378
8 cDNA enc	AAS41158	4	1868	82.1	1378
Muri	ADT49833	13	1338	•	1524
Full 16	ACF12809	8	2450		1536
	ADO01116	12	960	•	1608
	ADO01105	12	1378	97.2	1632
Ado01106 Human ser	AD001106	12	1375	97.2	1632
DNA enco	AAA57359	ω	2577	97.4	1635
Ado01092 Human ser	ADO01092	12	2554	•	1635
0	ACF12810	œ	2543	97.4	1635
51497	ABK51497	σ	2094	97.4	1635
3 Humar	AAL42458	σ	2040	97.4	1635
2 NSEQ s	AAZ52362	w	2040	97.4	1635
×	AAD23855	Φ	1797	97.4	1635
f16993		10	1583	97.4	1635
cDNA enco	7361	w	1563	97.4	ũ
001093 Human se	5	12	ω	97.4	ð
Ado01099 Human ser	ADO01099	12	1375	97.4	1635

## ALIGNMENTS

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ESULT 1
DJ11355
DJ11355
C ADJ11355;
X
C ADJ11355;
T 20-WAY-2004 (first entry)
X Human pRSS11-L cDNA encoding a serine protease SeqID 1.
X human; pRSS11-L; gene; ss; S2 serine protease; S2/HtrA; cellular physiology; apoptosis; gene therapy; osteoarthritis; papoptotic; osteopathic; antiarthritic; tranquiliser.
X Homo sapiens.
X Homo sapiens.
X Homo sapiens.
X Homo sapiens.
X US2004005659-A1.
X US2004005659-A1.
X US2004005659-A1.
X 03-JUL-2002; 2002US-00189099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel isolated nucleic acid molecule identified as PRSS11-L that encodes an S2 serine protease. Specifically, it refers to members of the S2/HtrA serine protease family, such that it plays a role in cellular physiology and apoptosis. The present invention provides agonists, antagonists, antibodies and recombinant expression vectors useful in methods of treatment, or detection and diagnosis of diseases associated with the abstrant expression or activity of the S2 serine protease, PRSS11-L. Accordingly, compositions described herein can be used via gene therapy routes to treat osteopathic, stress and apoptotic disorders. As such, they exhibit osteopathic, antiarthritic and tranquiliser activities. This polynucleotide sequence is the human PRSS11-L CDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated S2 serine protease nucleic acids and polypeptides, use for diagnosing and/or treating diseases with aberrant expression or activity the S2 serine protease, such as osteoarthritis, stress and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DARR/)
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ANDRADE-GORDON I
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              GlySerProPheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArg
GGCAGTCCCTTCGCCCTACAGAACACAGTGACAACGGGCATCGTCAGCACTGCCCAGCGG
                                                          CCTGTGTTGTTGCTGGGTCACTCGGCCGACCTGCGGCCTGGGGGAGTTTGTGGTGGCCATC
                                                                           ProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValValAlaIle
                                                                                                                     AAAGACATCGACAAGAAGTCGGACATTGCCACCATCAAGATCCCATCCCAAGAAAAAGCTC
                                                                                                                                           LysAspIleAspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLysLeu
                                                                                                                                                                                                  ProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGluAlaThrIle
                                                                                                                                                                                                                                           ATGTCAGAGGCCGGCCTGATCATCACCAATGCCCACGTGGTGTCCAGCAACAGTGCTGCC
                                                                                                                                                                                                                                                             MetSerGluAlaGlyLeuIleIleThrAsnAlaHisValValSerSerAsnSerAlaAla
                                                                                                                                                                                                                                                                                                                       PheLeuArgHisProLeuPheGlyArgAsnValProLeuSerSerGlySerGlyPheIle
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                                                                                                                                                                                                                                                                                                   The invention relates to TANGO polypeptide and its corresponding nucleic acid sequence. TANGO protein is used to identify a compound which binds to it that can be used for modulating its activity. It is also used to produce an antibody. The antibody is used to detect the presence of the polypeptide in a sample. TANGO DNA and protein are useful as modulating agents in regulating cellular processes. They can be used in vaccines. TANGO DNA and protein and its antibody are used in e.g. chromosomal mapping, tissue typing, forensic biology, predictive medicine, pharmacogenomics and treatment methods. TANGO DNA is used in antisense gene therapy. The present sequence is mouse TANGO DNA, Note: This sequence SEQ.ID.NO:9 is said to encode the protein AAEZ6441, but this is
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31-JUL-2000;
20-SEP-2000;
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                                                                                            ValLysValAsnGlyArgProLeuValAspSerSerGluLeuGlnGluAlaValLeuThr
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US-10-617-443B-2 (1-334) x ADO01091 (1-1359)
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                                                                                                                                                                                                                                                                                        The present invention relates to apoptosis inducers and protease inhibitors, which contain a compound inhibiting the activity or expression of human serine protease HTRA3 (ADD01199 and AD01115). The invention is useful for the treatment, prevention and diagnosis of pancreatic cancer, and also of other cancers including colon, breast, lung, prostate, oesophagus, stomach, liver, spleen, kidney, gall bladder, ovary, testis, bladder, thyroid and brain cancer and blood neoplasms. The present sequence is a coding sequence for HTRA3.
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27-JAN-2003; 2003JP-00017892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis inducers inhibiting activity or expression of serine protease HTRA3 for treatment, prevention and diagnosis of pancreatic cancer.
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                                                                         Human serine protease HTRA3 related DNA, SEQ ID
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Alignment & Pred. No.: Score:
                                                       The present invention relates to apoptosis inducers and protease inhibitors, which contain a compound inhibiting the activity or expression of human serine protease HTRA3 (ADO01090 and AD001115). The invention is useful for the treatment, prevention and diagnosis of pancreatic cancer, and also of other cancers including colon, breast, pancreatic, oesophagus, stomach, liver, spleen, kidney, gall bladd ovary, testis, bladder, thyroid and brain cancer and blood neoplasms. present sequence was used to illustrate the invention.
                                                      Sequence 1375 BP; 258 A; 447 C;
                                                                                                                                                                                                                                       Apoptosis inducers inhibiting activity or expression of serine protease HTRA3 for treatment, prevention and diagnosis of pancreatic cancer.
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     Example 3;
                                                 Apoptosis inducers inhibiting activity or expression of serine protease HTRA3 for treatment, prevention and diagnosis of pancreatic cancer.
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The present invention relates to apoptosis inducers and protease
CC inhibitors, which contain a compound inhibiting the activity or
CC invention of human serine protease HTRA3 (ADO01090 and ADO01115). The
CC invention is useful for the treatment, prevention and diagnosis of
CC pancreatic cancer, and also of other cancers including colon, breast,
CC lung, prostate, oesophagus, stomach, liver, spleen, kidney, gall bladder,
CC ovary, testis, bladder, thyroid and brain cancer and blood neoplasms. The
CC present sequence was used to illustrate the invention.

XX

Sequence 1378 BP; 259 A; 447 C; 430 G; 242 T; 0 U; 0 Other;
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CCC p	lung, prostate, oesophagus, stomach, liver, spleen, kilovary, testis, bladder, thyroid and brain cancer and be present sequence was used to illustrate the invention. Sequence 1378 BP; 259 A; 447 C; 430 G; 242 T; 0 U; 0 O mment Scores:  1.15e-159
음 성	0 LysIleAlaProAlaValValHisIleGluLeuPheLeuArgHisProLeuPheGl 
\$	50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleT
망	513 AACGTGCCCCTGTCCAGCGGTTCTGGCTTCATCATCATCAGAGGCCCGGCCTGATCATCAC
Ś	70 AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValO
片	573 AATGCCCACGTGGTGTCCAGCAACAGTGCTGCCCCGGGCAGCAGCAGCTCAAGGTGCAG
\$	euGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIleAspLysSerA
뭥	633 CTACAGAATGGGGACTCCTATGAGGCCACCATCAAAGACATCGACAAGAAGTCGGACATT
Ş	laThrIleLysIleHisProLysLysLysLeuProValLeuLeuClyHisS
망	693 GCCACCATCAAGATCCATCCCAAGAAAAAGCTCCCTGTGTTGCTTGC
Ś	130 AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnTh
DЪ	GCGGCCTGGGGAGTTTGTGGTGGC
Ś	150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAs
망	13 GTGAC
유 성	170 SerasphecasphyriledinfhraspalalielleasnfyrglyasnSerGlyglybrychellillillillillillillillillillillillilli
Ş	euValAs
В	933 CTGGTGAACCTGGATGGCGAGGTCATTGGCATCAACACGCTCAAGGTCACGGCTGGC
Ś	210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln
뭥	CCTTTGCCATCCCCTCAGACCGCATCACACGGTTCCTCACAGAGTTCCAAAG
Ş	230 IleLysAsgTrpLysLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeu
8	1053 ATCAAAGACTGGAAGAAGCGCTTCATCGGCATACGGATGCGGACGATCACACCAAGC
Ş	250 ValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIieTyrVa
Вb	TGGATGAGCTGAAGGCCAGCAACCCGGACTTCCCCAGAGGTCAGCAGTGGA

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RESULT 8
AAA57361
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XX AAAE
XX AAAE
XX HLT
XX HLT
XX HCT
XX AAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HtrA-2; high temperature requirement A-2 protein; TANGO 219; arthritis; bone disorder; cartilage disease; bone breakage; cartilage tearing; osteoporosis; osteoarthritis; bone wearing; ischemic heart disease; atherosclerosis; hyperplasia; ventricular fibrillation; visceromegaly; placentomegaly; cardiac defect; Beckwith-Weidermann syndrome; cancer; cellular migration; cell proliferation; serine protease; Alzheimer's disease; multiple sclerosis; Huntington's disease; parkinson's disease; neurodegeneration; frontal lone dementia; cortical lewy body disease; acquired immunodeficiency syndrome; AIDS; dementia; chronic epilepsy; adipocyte function; heart disease; ischemic heart disease; ventricular fibrillation; myocardial infarction; ischemic heart disease; ventricular fibrillation; myocardial infarction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProGluValValMet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a HtrA-2 (high temperature requirement A-2) protein
                                                                                     98US-00224246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "HtrA-2 (high temperature requirement A-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variation is present are absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace(396,C)
/*tag= b
                                                                                                                                                                                                                                                                                      variation is present are absent"
                                                                                                                                                                                                                                                                                                                                                                                         variation is present are absent" replace(498,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/*tag= c
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variation is present only when
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "the encoded amino
variation is present only
                                                                                                                                                                                                                                                                                                                                            /note= "the encoded
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Novel human high temperature requirement-2 and TANGO 219 secreted proteins and nucleic acids encoding them which are useful for treating atherosclerosis, placentomegaly, cancer, Alzheimer's disease and
                                                                                                                                                   Claim 2; Fig 8A-C; 122pp;
                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                              Barnes
                                                                                                                                                                                                  2000-452366/39.
                                                                                                                                                                                                              X
                                                                                                                                                                                             AAY93963.
                                                                                                                                                    English
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The present sequence encodes a murine HtrA-2 (high temperature crequirement A-2) protein. The specification also describes TANGO 219 polypeptides. HtrA-2 nucleic acid, proteins and its modulators can be used to treat bone and/or cartilage associated diseases or disorders. CC e.g. bone breakage, cartilage tearing, osteoporosis, arthritis, cc heart disease, atherosclerosis, hyperplasia, and ventricular cc fibrilation. HtrA-2 can also modulate IGF function and can be used to freat visceromegaly, placentomegaly, cardiac and adrenal defects, cc seckwith-Weidermann syndrome, and cancer. It is useful to treat disorders cc involving abnormal cellular migration, proliferation. HtrA-2 acts as a cc involving abnormal cellular migration, proliferation. HtrA-2 acts as a crime protease and can be used to treat Alzheimer's disease. HtrA-2 can also be used to treat multiple sclerosis, Huntington's disease. HtrA-2 can lewy body disease, neurodegeneration, frontal lone dementia, cortical lewy body disease, acquired immunodeficiency syndrome (AIDS), dementia can modulate adipocyte function and adipocyte-related processes and can chronic epilepsy. HtrA-2 nucleic acids, proteins and its modulators can modulate adipocyte function and adipocyte-related processes and ce.g., ischemic heart disease or atherosclerosis, or cerebrovascular cc e.g., ischemic heart disease or atherosclerosis, or cerebrovascular convolving heart contraction, and the impulse generating conditions cc involving heart contraction, and the impulse generating nodes and cardiac and cancel cells, e.g. ventricular fibrillation or myocardial infarction

Sequence 1563 BP; 337 A; 462 C; 458 G; 306 T; 0 U; 0 Other;

Percent Similarity:
Best Local Similarity:
Query Match:

1.36e-159 1635.00 100.00% 100.00% 97.38%

Gaps: Indels:

Length: Matches: Conservative: Mismatches:

1563 325 0 0

No : :

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                           AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr
                                                                                                                                                                      AAGATCGCACCAGCCGTGGTCCACATAGAGCTCTTCCTGAGACACCCGCTGTTTGGCCGC
AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr
                                                                       LeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIleAspLysLysSerAspIle
                                                                                                       AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGln 89
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RESULT 9
ACF12
ACF1
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03-MAY-2001; 2001US-0288935P
07-MAY-2001; 2001US-028903PP
08-MAY-2001; 2001US-0289620P
08-MAY-2001; 2001US-0289621P
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2001US-0292587P.
2001US-0293107P.
2001US-0293589P.
2001US-0294174P.
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## CURAGEN CORP.

Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Casman & Eddinger SR, Ellerman K, Gangolli EA, Gerlach VL, 'Gorman L, Gunther E, Herrmann JL, Ji W, Lepley DM, Lewin DA, Li L; Macdougall JR, Malyankar UM, Mezes PD, Padigaru M, Pattura Peyman JA, Rastelli L, Rieger DK, Rothenberg ME, Shenoy SC Smithson G, Spytek KA, Stone DJ, Taupier RJ, Tchernev VT; Vernet CAM, Voss EZ, Zerhusen BD, Zhong H, Miller CE; M. Patturajan ខ្ម Z

## 2003-111987/10.

New NOVX polypeptides and polynucleotides useful for treating or preventing e.g. cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect, or atrioventricular

Claim 20; Page 197; 491pp; English

ACF16939 to ACF17000 encode the human G protein-coupled receptor (GPCR) CC proteins, designated NOVX proteins, given in ABR96130 to ABR96191. The CO NOVX sequences can have cytostatic, cardiovascular, antiasthmatic, immunosuppressive, anti-HIV (human immunodeficiency virus), hypotensive and antiarteriosclerotic activities, and can be used in gene therapy. NoVX polypeptides can be used to treating a syndrome associated with a comman disease such as a pathology associated with the polypeptide. NOVX polypeptides, polymucleotides and antibodies can be used for treating or preventing e.g. cardiomyopathy, atherosclerosis, hypertension, congenital cheart defects, pulmonary stenosis, atrial septal defect, atrioventricular canal defect, pulmonary stenosis, prostate cancer, uterine cancer, neoplasm, graft versus host disease, acquired immunodeficiency syndrome (AIDS), Crohn's disease, multiple sclerosis, or bronchial asthma. The nucleic acid sequences may be used in promosome mapping, identifying individual from minute biological samples (tissue typing), and in represent PCR primers and probes for the NOVX sequences, which are used an the present

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AAD23855 standard; cDNA; 1797
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                                                         PRTS-14 cDNA
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Human; protease; PRTS-14; tranquilliser; gene therapy; vaccine; allergy; infection; dermatitis; arteriosclerosis; rheumatoid arthritis; hepatitis; atherosclerosis; psoriasis; Alzheimer's disease; mental disorder; cancer; gastrointestinal disorder; Cushing's syndrome; setzure; glaucoma; stroke; epithelial disorder; urticaria; anorexia; trauma; asthma; eczema; nausea; hypertension; neurological disorder; Parkinson's disease; drug screening; cardiant; cell proliferative disorder; multiple sclerosis; osteoporosis; diabetes mellitus; glomerulonephritis; cardiovascular disorder; anaemia; autoimmune disorder; inflammatory disorder; myocardial infarction; AIDS; developmental disorder; reproductive disorder; infertility; diarrhoea; dementia; acidosis; cataract; gynaecomastia; epilepsy; jaundice; ss.

Homo sapiens.

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mat_peptide
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  "Mature human protease PRTS-14 protein"
                                                            "Human protease PRTS-14 protein"
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WO200183775-A2

04-MAY-2000; 2000US-0202082P. 11-MAY-2000; 2000US-0203566P. 17-MAY-2000; 2000US-0205803P. 25-MAY-2000; 2000US-0207477P. 01-JUN-2000; 2000US-0209402P. 04-MAY-2001; 2001WO-US014651

(INCY-) INCYTE GENOMICS

Delegeane Tribouley Nguyen Reddy F n DB, c. R. Yue H, ₽,¥ Gandhi AR, Lal P, H Khan FA, Hafalia A, YT; Yao MG, Yang J, , Patterson C, Walia NK, Kearney Baughn MR, Azimzai Y, Elliott V Hernandez R, Policky JL, Lu DAM; ٧s;

WPI; 2002-034518/04. P-PSDB; AAE14349.

Novel human proteases and polynucleotides encoding the proteases, useful for treating, diagnosing or preventing cell proliferative, cardiovascular, autoimmune/inflammatory, neurological and developmental

Claim 5; Page 150-151; 151pp; English

The invention relates to human proteases (PRTS1-14) and its corresponding CDNA molecules. Human PRTS and its nucleic acid molecule are useful for the diagnosis, treatment and prevention of disorders associated with increased or decreased expression of PRTS. Examples of such disorders include, cell proliferative disorders (arteriosclerosis, atherosclerosis, hepatitis, psoriasis and cancers); autoimmune/inflammatory disorders (AIDS, Addison's disease, allergy, anaemia, asthma, atopic dermatitis, diabetes mellitus, glomerulonephritis, multiple sclerosis, osteoporosis, trauma, Grave's disease, rheumatoid arthritis, ulcerative colitis, and viral, bacterial, parasitic, protozoal and helminthic infections); cardiovascular disorders (myocardial infarction, ischaemic heart

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Crohn's disease, anorexia, nausea, diarrhoea and jaundice); epithelial disorders (contact dermatitis, eczema, acne vulgaris, alopecia, scabies, insect bites and urticaria); reproductive disorder (infertility, disruption of estrous and menstrual cycle and gynaecomastia); and developmental disorders (renal tubular acidosis, Cushing's syndrome, seizure disorders, congenital glaucoma and cataract). PRTS DNA is also in useful is gene therapy. PRTS and its immunogenic fragments are useful for screening libraries of compounds in several drug screening assays. The present sequence is human protease PRTS-14 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease and hypertension); neurological disorders (epilepsy, Alzheim disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease, stroke, mental disorders including mood, anxiety and season affective disorder and prion diseases); gastrointestinal disorders
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                                                                                                                                                                Protein co-expressed with matrix-remodeling proteins, useful in diagnosis and treatment of cancer, cardiomyopathy, arthritis, angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSEQ gene; matrix-remodeling gene; Incyte clone 2814981; cancer; matrix-remodeling disease; cardiomyopathy; arthritis; angiogenesis; diabetic necrosis; atherosclerosis; fibrosis; ulceration; cytostatic; cardioactive; antiarthritic; angiogenic; antiarteriosclerotic; antiulcer;
                                                                                              Claim
                                                                                                                                            angiogenesis, ulceration.
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The present sequence is NSEQ gene that is co-expressed with one known matrix-remodeling genes in a number of biological samples expression vector. This sequence was identified from the Incyte

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                                                     The invention comprises human nucleotide sequences which are co-expressed with matrix-remodeling genes. Matrix-remodeling is associated with the construction, destruction and reorganisation of extracellular matrix components. The matrix-remodeling-associated nucleotides of the invention are useful for screening for and purifying ligands that specifically bind to the nucleotides of the invention. The matrix-remodelling-associated nucleotides of the invention are also useful in the diagnosis, prognosis, prevention, treatment and evaluation of therapies for diseases associated with matrix remodelling (e.g. angiogenesis, arthritis, atherosclerosis, cancer, cardiomyopathy, diabetic necrosis, fibrosis and ulceration). The present DNA sequence represents a human matrix-remodeling-associated nucleotide of the invention
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                                      GAGTCTCCTCTCCTACTGGAGGTGCGGCGGGGGAACGACCTCCTCTTCAGCATCGCA
                                                       GluSerProLeuLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAla
                                                                                                                                         CAAGAGGTTGCGCCGAATTCACCTTCTCAGAGAGGCGGCATCCAAGATGGTGACATCATC
                                                                                                                                                                                                                                                           SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln
                                                                                                                                                                                                                                                                                                                                                 CTGGTGAACCTGGATGGCGAGGTCATTGGCATCAACACGCTCAAGGTCACGGCTGGCATC
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RESULT 13
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                                                      The invention relates to isolated human polypeptides designated LP102, CC LP187, LP190 and LP241, and the polynucleotides encoding them. The LP polypeptide or the LP polypeptide agonist is useful for treating a mammal CC suffering from a disease, condition or disorder associated with aberrant levels of an LP polypeptide. The LP polypeptides or polynucleotides, or CC inflammatory disorders, bone diseases or cardiovascular diseases. In CC particular, the LP102 polypeptides, polynucleotides or antibodies are useful for diagnosing, preventing or treating male reproductive system CC diseases, osteoporosis, Paget's disease, metastatic or myeloma associated bone diseases or Alzheimer's disease, metastatic or myeloma associated contraceptive agents. The LP187 polypeptides, polynucleotides or antibodies are useful for diagnosing, preventing or treating preventing or treating cancer, as well as other growth factor-mediated diseases and CC useful for diagnosing, preventing or treating asthma, anaphylaxis, and CC useful for diagnosing, preventing or treating asthma, anaphylaxis, and CC diseases related to coagulation or sepsis. LP241 polypeptides, polynucleotides are useful for diagnosing, preventing or treating asthma, anaphylaxis, and CC useful for the LP polynucleotides are useful especially for diagnosing, preventing or treating sethma, anaphylaxis, and CC useful for the LP polynucleotides are useful especially for diagnosing, preventing or treating sethma anaphylaxis and vectors that may be employed in medicine, or for preparing the proteins. The present sequence represents the coding sequence of LP241
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US-10-617-443B-2 (1-334) x ACF12810 (1-2543)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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2003JP-00017892
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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              US-09-949-016-4643
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US-08-923-454A-17
US-08-923-454A-7
US-08-923-454A-7
US-08-923-454A-23
US-08-923-454A-24
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## ALIGNMENTS

RESULT 1 US-09-949-016-4643

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Percent Similarity:
Best Local Similarity:
Query Match:
US-10-617-443B-2 (1-334) x US-09-949-016-4643 (1-1521)
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SOFTWARE: FASESEQ for W
SEQ ID NO 4643
LENGTH: 1521
TYPE: DNA
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Sequence 399, Application Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Cra
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VENTER, J. Craig
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                                                                                                                 GCGTATATAATTGAAGTAATTCCTGATACCCCAGCAGAAGCTGGTGGTCTCAAGGAAAAC
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
LysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
                                                                                                                                               GlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeu 203
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RESULT 3
US-08-888-077A-41
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                                                                                                                                                                                       TELEFAX: (908) 654-7866 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE-OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFY
                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,629
REFERENCE/DOCKET NUMBER: SCI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 41
CORRESSES: LERNER, DAVID, LIT-
ADDRESSES: LERNER, DAVID, LIT-
STREET: 600 SOUTH AVENUE WEST
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 00 FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION: NAME: PALISI, THOMAS M
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                             FEATURE:
                               NAME/KEY: misc_fer
LOCATION: 1.2205
OTHER INFORMATION:
                                                                                                           LENGTH: 2205 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 03-JUL-1997
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                                   /note= "mutTM1-TM2"
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                                 SerGluLeuGluGluAlaValLeuThrGluSerProLeuLeuLeuGluValArgArgGly 320
                                                                                                                                                                           ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg
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                                                                         ĠĠŦĠĠŦĊŦĊAAGGAAAACĠĀĊĠŦĊĀŦĀAŦĊAGĊAŦĊĀAŦĠĠĀĊAĠŦĊĊĠŦĠŦĊŦĊĊĠĊĊ 1459
                                                                                                           GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer 300
                                                                                                                                                     CCAGACGTGATCTCAGGAGCGTATATAATTGAAGTAATTCCTGATACCCCAGCAGAAGCT 1399
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ATTORNEY AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P505
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2036 base pairs
TYPE: nucleic acid
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APPLICANT: Livi, George
APPLICANT: Karran, Eric
                                                                                                                                                          Local Similarity:
                                                                                                                                                                                                                                                                              ORIGINAL SOURCE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
PRIOR APPLICATION NUMBER: 60/025436
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SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               No.:
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
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APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE
NUMBER OF SEQUENCES: 40
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CITY: K
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Sequence 22, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Mutison, James D
APPLICANT: Mutison, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for t
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                                                                                                                                                                                                                                                                                 SerGluLeuGlnGluAlaValLeuThrGluSerProLeuLeuGluValArgArgGly 320
                                                                                                                                                                                                                                                                                                                    GKTGGTCTCAAGGAAAACGACGTCATAATCAGCATCAATGGACAGTCCGTGGTCTCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                     ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIle 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGGACTGATCGTGACAAATGCCCCACGTGGTGACCAAC-------AAG
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REFERENCE:

11000.1050U1

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LENGTH: 1859
TYPE: DNA
ORGANISM: Mouse
US-09-724-864-22
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 22
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CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 63803
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
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nLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAl
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                                                  ### AGACTATATCCAGACGGATGCCATCATTAACCATGGAAATTCTGGGGGTCCGCTGGTGAA
                                                                      tAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAs
                                                                                                                                                                                                 gProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrTh 152
                                                                                                                                                                                                                                                                     eLysIleHisProLysLysLysLeuProValLeuLeuGlyHisSerAlaAspLeuAr 132
                                                                                                                                                                                                                                                                                                                                 CGTCCTCACCAAC----
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|GTGGTCCACTTGCAGCTGTTCCGCAGATGACAGACACACAGGTTCCCCACACTGATCTAAA 242
                                                                                                                  AGGGATTGTCAGCACCACACAGAGAGGGGGGGGAGAGGCTGGGACTGAAGAATTCAGACAT
                                                                                                                                             rGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMe 172
                                                                                                                                                                                                                                                                                                               CGGGGCCCGGTATGAAGCCACCGTCAAAGACATCGACCATAAACTGGACCTTGCACTGAT
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                                                                                                                                                                                                                                               TAAGATCGAGCCAGATACTGAGCTTCCAGTACTGCTGCTGGGCCGATCCTCTGACCTCCG
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1999-12-23
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Matches:
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                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 base pair
                                                                                  REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Southan, Christopher TITLE OF INVENTION: HUMAN SERINE NUMBER OF SEQUENCES: 40
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                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                     TELEFAX: 610-270-5090
                                                                                                                                                          NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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CAAGGCCCCTTTGCAGAAGAAATACCTGGGTCTTCGAATGCTGCCTCTCACTCTGAACCT 944
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Livi, George
Karran, Eric
Clinkenbeard,
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SYSTEM: DOS
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
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OTHER INFORMATION:
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AspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrValGln 270
                                                                                                                     SerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln------Ile
                                                                                                                                                                                                                ATTCAAACTGATGCAGCTATTGATTTTGGAAACTCTGGAGGTCCCCTGGTTAACCTGGAT
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                              AGTGGGTCCCAGCGCCTACATTGGGGTGATGATGCTGACCCTGAGTCCCAGCATCCTT
                                                        LysaspTrpLysLysargPheIleGlyIleargMetargThrIleThrProSerLeuVal
                                                                                          TCTGATCGTCTTCGAGAGTTTCTGCATCGTGGGGAAAAGAAGAATTCCTCCTCCGGAATC
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APPLICANT: ZETVOS, ANTONIS S.

ITTLE OF INVENTION: CELL PROLIFERATION RELATED GEI
FILE REFERENCE: 10284/004001

CURRENT APPLICATION UNWBER: US/09/075,460A

CURRENT FILING DATE: 1998-05-08

EARLIER APPLICATION NUWBER: US 60/046,077

EARLIER FILING DATE: 1997-05-09

NUMBER OF SEQ ID NOS: 16

SOPTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4
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TYPE: DNA
ORGANISM: Homo :
FEATURE:
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                                                               SerTyrGluAlaThrIleLysAspIleAspLysLysSerAspIleAlaThrIleLysIle 114
                                                                                                                     SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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APPLICANT:
APPLICANT:
                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett COMPUTER: IBM Compat
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
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                                                                                                                                                                  CITY: King of Prussia
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                                                                                                                                                                                        3: SmithKline Beecham Corporation
709 Swedeland Road
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Livi, George
                                   IBM Compatible SYSTEM: DOS
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Clinkenbeard, Helen
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/0 FILING DATE: 06-SEPT-199 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 603...1976
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                     GTTAGCTCTGCTCAGCGTCCAGCCAGAGACCTGGGGACTCCCCCAAACCAATGTGGAATAC
                                                       ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyr 174
                                                                                                                                                                                                                                                ACGTATGAGGCCGTGGTCACAGCTGTGGATCCCCGTGGCAGACATCGCAACGCTGAGGATT
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Matches:
Conservative:
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Indels:
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RESULT 9
US-08-923-454A-24
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APPLICATION NUMBER: US/08/923,4:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumedister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                           STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, H
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 709 Swedeland CITY: King of Prussia
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Clinkenbeard, Helen
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Best Local Similarity:
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LENGTH: 2187 base pairs
TYPE: nucleic acid
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OTHER INFORMATION:
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TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aacggcTcaggaTTcGTGgTGGCTGCCGATGGGCTCATTGTCACCAACGCCCATGTGGTG
                                                                                    GGGGAGGTGATTGGAGTGAACACCATGAAGGTCACAGCTGGAATCTCCTTTGCCATCCCT
                                                                                                                                                                                                                                                                                                                                                       GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
                                                                                                                                                                                                                                                                                                                                                                                                                                 HisProLysLysLysLeuProValLeuLeuGlyHisSerAlaAspLeuArgProGly
                                     SerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln-----
                                                                                                                                                                  ATTCAAACTGATGCAGCTATTGATTTTGGAAACTCTGGAGGTCCCCTGGTTAACCTGGAT
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                                                                                                                                                                                                                                                                              ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyr 174
                                                                                                                                                                                                                                                                                                                                  GAGTTTGTTGTTGCCATGGGAAGTCCCTTTGCACTGCAGAACACGATCACATCCGGCATT
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      TCTGATCGTCTTCGAGAGTTTCTGCATCGTGGGGAAAAGAAGAATTCCTCCTCCGGAATC
                                                                                                             GlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIlePro
                                                                                                                                                                                             IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
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RESULT 10
US-09-008-271A-23
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Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
                                                                                                TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REPERENCE/DOCKET NUMBER: PF-0458 US
TELEPOMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                   IMMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN PROTEASE MOLECULES NUMBER OF SEQUENCES: 24
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                                              LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FREUSEQ for Windows Version
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                                TOPOLOGY: linear
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Corley, Neil C.
Tang, Tom Y.
                SOURCE:
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Thah, Purvi
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                                                                                                                                    GCTGAACTACAGCTTCGAGAACCAAGCTTTCCCGATGTTCAGCATGGTGTACTCATCCAT
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US-08-923-454A-30
        Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                            US-08-923-454A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 2187 base pairs
TYPE: nucleic acid
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APPLICANT:
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Baumeister, Kirk REGISTRATION NUMBER: 33,833 REGISTRATION NUMBER: P5
TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923
                                                                                                                                                                             HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
CRIGINAL SOURCE:
POlymorphic variants at 672 and 1435
FEATURE: Polymorphic variants at 672 and 1435
FEATURE: a224=Arg/Cys
RAME/KEY: Coding Sequence
LOCATION: 603...1976
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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О.:
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Livi, George
Karran, Eric
Clinkenbeard, I
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Matches:
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Gaps:
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US-08-923-454A-3
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US-10-617-443B-2 (1-334) x US-08-923-454A-3 (1-1787)
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                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                             US-08-923-454A-3
                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08923454A Patent No. 6004794
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APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/02:
PILLING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Creasy, Caretha APPLICANT: Livi, George APPLICANT: Karran, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CON
OPERATING SYSTEM:
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            Sequence 26, Application US/08923454A Patent No. 6004794
GENERAL INFORMATION:
                                                                                                 1381 CAGATCCGGCGGGACGAGAAACACTGACCTTATATGTGACCCCTGAGGTC 1431
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                                                                                                                                                                   ATGGTACAAAATGCTGAAGATGTTTATGAAGCTGTTCGAACCCAATCCCAGTTGGCAGTG
                                                                                                                                                                                                                                                                                                                               SerAsnProAspPheProGluValSerSerGlyIleTyrValGlnGluValAlaProAsn
                                                                                                                                                                                                                                                                                                                                                                                             ArgPheIleGlyIleArgMetArgThrIleThrProSerLeuValAspGluLeuLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HisProLysLysLysLeuProValLeuLeuGlyHisSerAlaAspLeuArgProGly
                                                                                                                                 GluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaProGluVal 332
                                                                                                                                                                                                                                                                    SerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArg
                                                                                                                                                                                                                                                                                                          CGAGAACCAAGCTTTCCCGATGTTCAGCATGGTGTACTCATCCATAAAGTCATCCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTTTCTGCATCGTGGGGAAAAGAAGAATTCCTCCTCCGGAATCAGTGGGTCCCAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGAACACCATGAAGGTCACAGCTGGAATCTCCTTTTGCCATCCCTTCTGATCGTCTTCGA 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGACTAAGGAGCCTCTCCCCACGCTGCCTCTGGGACGCTCAGCTGATGTCCGGCAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGTATGAGGCCGTGGTCACAGCTGTGGATCCCGTGGCAGACATCGCAACGCTGAGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerTyrGluAlaThrIleLysAsplleAspLysLysSerAsplleAlaThrIleLysIle 114
                                                                                                                                                                                                     ProLeuValAspSerSerGluLeuGlnGluAlaValLeuThrGluSerProLeuLeuLeu 315
                                                                                                                                                                                                                                      TCCCCTGCACACCGGGCTGGTCTGCGGCCTGGTGATGTGATTTTGGCCATTGGGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                           CGCTACATTGGGGTGATGCTGACCCTGAGTCCCAGCATCCTTGCTGAACTACAGCTT 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgPheLeuThrGluPheGlnAspLysGln-----IleLysAspTrpLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATTTGTTTAGGCTAGGGAACTGGGGGGCTGTATCCCTGCAGGATGGGGAGGTGATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCTAATTCAAGGATGTTTGGTCAAGTTTCTGAGCAGTTCTTTGTTGGCTATCTCTCAA. 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGAGACATCCTTCCTTCCAAGAATCCCTGCCCCAGGTCAGTGTGGGAAGGGTAGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTAGCTCTGCTCAGCGTCCAGCCAGAGACCTGGGGACTCCCCCCAAACCAATGTGGAATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTCAAACTGATGCAGCTATTGATTTTGGAAACTCTGGAGGTCCCCTGGTTAACCTGGTG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CGGCGCAGAGTCCGTGTGAGACTGCTAAGCGGCGAC
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193

193

193

660

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720

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APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Exic
APPLICANT: Clinkenbeard, Helen
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
COUNTRY: ***
                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                         US-08-923-454A-26
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INFORMATION FOR SEQ ID NO: 26

SEQUENCE CHARACTERISTICS:

LENGTH: 2551 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
SOFTMARE: FASTSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/08/923,454A
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELEPHONE: 610-270-5096
TELEPHONE: 610-270-5096
TELEPAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: FEATURE: Coding Sequence NAME/KEY: Coding Sequence LOCATION: 603...1733
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19406
                                                                                                                                          1083
                 1143
                                                                                                 35 ValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
                                              5
           SerGlySerGlyPhelleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValVal 74
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AACGGCTCAGGATTCGTGGCTGCCGATGGGCTCATTGTCACCAACGCCCATGTGGTG 1202
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834.50
60.71%
42.57%
49.70%
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Matches:
Conservative:
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Indels:
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169
72
71
85
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                           RESULT 14
US-08-923-454A-5
; Sequence 5, Application US/08923454A
; Patent No. 6004794
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	316 GluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaProGluVal 332	Ş
EET2 61	2085 ATGGTACAAAATGCTGAAGATGTTTATGAAGCTGTTCGAACCCAATCCCAGTIGGCAG	Db
315	296 ProLeuValAspSerSerGluLeuGlnGluAlaValLeuThrGluSerProLeuLeuLeu	Q
, ,	2025 TCCCCTGCACACCGGGCTGGTCTGCGGCCTGGTGATGTGATTTTTGGCCAIIGGGGATGT	Дb
	276 SerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArg	Ş
) i	1965 CGAGAACCAAGCTTTCCCGATGTTCAGCATGGTGTACTCATCCATC	망
3n 275	256 SerAsnProAspPheProGluValSerSerGlyIleTyrValGlnGluValAlaProAsn	S S
3 6	1905 CGCTACATTGGGGTGATGCTGACCCTGAGTCCCAGCATCCTTGCTGAACTACAGC	В
1964	236 ArgPheIleGlyIleArgMetArgThrIleThrProSerLeuValAapGluLeuLy8ALA	S
, ,	1845 GAGTTTCTGCATCGTGGGGAAAAGAAGAATTCCTCCTCCGGAATCAGTGGGTCCCAGCG	DЬ
	220 ArgPheLeuThrGluPheGlnAspLysGlnIleLysAspTrpLysLys	Ś
) h	1785 GTGAACACCATGAAGGTCACAGCTGGAATCTCCTTTTGCCATCCCTTCTGATCGTCTTCG	ఠ
219	200 IleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThr	Q
-	1725 CTATTTGTTTAGGCTAGGGAACTGGGGGCTGTATCCCTGCAGGATGGGGAGGTGATTGG	D D
199	194AspGlyGluValIleGly	Ş
	1665 TATCCAACCAGATCTCCCCAACACTTGCTGGTACTTTTGTTCGGGTGCCCCCATCCCCTA	망
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	1485 ATTCAAACTGATGCAGCTATTGATTTTGGAAACTCTGGAGGICCCCIGGIAACCTCTGGAAGACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTCTGGAAGAACTGAAACTAACT	В
193	175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeu	Ş
	1425 GTTAGCTCTGCTCAGCGTCCAGCCAGAGACCTGGGACTCCCCCCAAACCAATGTGGAATAC	Db
174	155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyr	S
ш	1365 GAGTTTGTTGCCATGGGAAGTCCCTTTTGCACTGCAGAACACGATCACATCCGGCATT	Дb
15	135 GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle	γQ
13	1305 CAGACTAAGGAGCCTCTCCCCACGCTGCCTCTGGGACGCTCAGCTGATGTCCGGCAAGGG	타
13	115 HisProLysLysLysLeuProValLeuLeuGlyHisSerAlaAspLeuArgProGly	Ş
1304	1245 ACGTATGAGGCCGTGGTCACAGCTGTGGATCCCGTGGCAGACATCGCAACGCTGAGGATT	дb
114	95 SerTyrGluAlaThrIleLy8AspIleAspLy8Ly8SerAspIleAlaThrIleLy8Ile	Ş
	1203 GCTGAT	뭥
94	75 SerSerAanSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAanGlyAsp	Ş

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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                            JS-08-923-454A-5 ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Baumeister, Kirk REGISTRATION NUMBER: 33,883 REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/02 FILING DATE: 06-SEPT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                502 AACGGCTCAGGATTCGTGGTGGCTGCCGATGGGCTCATTGTCACCAACGCCCATGTGGTG
                                                                                                                                                                                    382 GCTTCTCCCCGGAGTCAGTACAACTTCATCGCAGATGTGGTGGAGAAGACAGCACCTGCC
                                                                                                                   442 GTGGTCTATATCGAGATCCTGGACCGGCACCCTTTCTTGGGCCGCGAGGTCCCTATCTCG
                   75
                                                                                                                                                 35 ValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAsp
                                                                         SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValVal
                                                                                                                                                                                                     SerSerProArgTyrLysPheAsnPheIleAlaAspValValGluLysIleAlaProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T: Southan, Christopher INVENTION: HUMAN SERINE PROTEASE
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Browne, Michael
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Karran, Eric
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                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Creasy
APPLICANT: Livi,
                                                                                                                 APPLICANT: Southan, Christopher TITLE OF INVENTION: HUMAN SERINE PROTEASE
                                                                                                                                                                  APPLICANT:
                                                                              CORRESPONDENCE ADDRESS:
                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                  APPLICANT:
STATE: P
               CITY: King of Prussia STATE: PA
                                               STREET:
                                                                  ADDRESSEE:
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                                                  709
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Clinkenbeard, Helen
Browne, Michael
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ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat

IBM Compatible

Diskette

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 2144 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P505
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-270-5996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE: FEATURE:
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SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06-SEPT
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                                                                                                                                   SerTyrGluAlaThrIleLy8AspIleAspLysSerAspIleAlaThrIleLy8Ile 114
                                                                                                                                                                                                    SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAsp 94
                                                                HisProLysLysLysLysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGly 134
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| GCTGGTCTGCGGCCTGGTGATTGTGATTTTGGCCATTGGGGAGCAGATGGTACAAAATGCT 1808
                                                                                                     GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer
CGAGAAACACTGACCTTATATGTGACCCCTGAGGTC 1904
                  AsnAspAspLeuLeuPheSerIleAlaProGluVal
                                         GAAGATGTTTATGAAGCTGTTCGAACCCAATCCCAGTTGGCAGTGCAGATCCGGCGGGA
                                                       SerGluLeuGlnGluAlaValLeuThrGluSerProLeuLeuLeuGluValArgArgGly
                                                                                                                                                ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg
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Search completed: June 30, Job time : 320.971 secs 2005, 01:32:59

sequence:

Title:

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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-DB=Published_Applications_NA -QFMT=fastap_SUBFTIX=rnpb-MINMATCH=0.1
-LOOPECL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -WATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCCALICN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -WODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=USI0617443 @CGN 1 1 582 @runat 29062005 135933 26126
-NCPU=6 -ICPU=3 -NO_MMAp -LARGEQUERY -NCEG SCORES=0 -WAIT -DSPBLOCK=100 -
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Ygapop 10.0 , Y
Fgapop 6.0 , F
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6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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                                                                       _6/ptodata/1/pubpna/US101_PUBCOMB.seq:
_6/ptodata/1/pubpna/US10 NEW PUB.seq:
_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:
_6/ptodata/1/pubpna/US11NEW PUB.seq:
_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
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1/pubpna/US09C PUBCOMB.seq:*
1/pubpna/US09 NEW PUB.seq:*
1/pubpna/US10A PUBCOMB.seq:*
1/pubpna/US10A PUBCOMB.seq:*
1/pubpna/US10C PUBCOMB.seq:*
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Database :

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Query Match Length DB

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Description

## ALIGNMENTS

GENERAL INFORMATION:
APPLICANT: Darrow, Andrew L
APPLICANT: Qi, Jian-shen
APPLICANT: Qi, Jian-shen
APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Human PRSS-11 like S2 ser
FILE REFERENCE: ORT-1644
CURRENT APPLICATION NUMBER: US/10/189,099A
CURRENT FILING DATE: 2002-12-10 US-10-189-099A-1 Sequence 1, Application US/10189099A Publication No. US20040005659A1 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PatentIn Ver. EQ ID NO 1 2.1 S2 serine protease and uses thereof

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Best Local Similarity:
Query Match:
DB:
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; TYPE: cDNA
; ORGANISM: Homo sapiens
US-10-189-099A-1
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                                                  ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg
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CURRENT APPLICATION NUMBER: US/10/617,443B
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3006
TYPE: DNA
CORGANISM: Homo sapiens
US-10-617-443B-1
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US-10-617-443B-1
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Publication No. US20050019777A1
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew L
APPLICANT: Qi, Jian-shen
APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
FILE REFERENCE: ORT-1644
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RESULT 3
US-09-796-858-9
                                                   PRIOR APPLICATION NUMBER:
PRIOR PILING DATE: 1998-12
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-12
PRIOR PILING DATE: 1998-12
PRIOR PILING DATE: 1999-12
PRIOR PILING DATE: 1999-05
PRIOR APPLICATION NUMBER:
PRIOR PILING DATE: 1999-06
PRIOR APPLICATION NUMBER:
PRIOR PILING DATE: 1999-06
PRIOR PILING DATE: 1999-06
PRIOR PILING DATE: 1999-09
PRIOR PILING DATE: 1999-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09796858
Patent No. US20020055139A1
GENERAL INFORMATION:
APPLICANT: Holtzmann, Douglas
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC,
TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
EXIT PETEROPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/796,858
CURRENT FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 7853-226-999
                                                 DR FILING DATE: 1999-06-29
DR APPLICATION NUMBER: 09/39
DR FILING DATE: 1999-09-20
DR APPLICATION NUMBER: 09/47
DR FILING DATE: 1999-12-23
DR APPLICATION NUMBER: 09/47
DR FILING DATE: 1999-12-29
DR APPLICATION NUMBER: 09/47
DR FILING DATE: 1999-12-29
DR APPLICATION NUMBER: 09/47
DR FILING DATE: 1999-12-29
DR APPLICATION NUMBER: 09/57
DR FILING DATE: 1999-12-29
DR APPLICATION NUMBER: 09/57
DR FILING DATE: 2000-05-14
DR APPLICATION NUMBER: 09/59
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DR FILING DATE: 1998-12-30
DR APPLICATION NUMBER: 09/22
DR FILING DATE: 1998-12-30
DR APPLICATION NUMBER: 09/31:
DR FILING DATE: 1999-05-14
DR APPLICATION NUMBER: 09/33
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Best Local Similarity:
Query Match:
DB:
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                                       IleLysAspTrpLysLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeu
                                                                                                                 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln
                                                                                                                                                                                          LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIle
                                                                                                                                                                                                                                                                        SerAspMetAspTyrI1eG1nThrAspAlaI1eI1eAsnTyrG1yAsnSerG1yG1yPro
                                                                                                                                                                                                                                                                                                                         GTGACAACGGCATCGTCAGCACTGCCCAGCGGGAGGGCAGGGAGCTGGGCCTCCGGGAC
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                                                                                                                                                                    CTGGTGAACCTGGATGGCGAGGTCATTGGCATCAACACGCTCAAGGTCACGGCTGGCATC
                                                                                                                                                                                                                                                  TCCGACATGGACTACATCCAGACGGATGCCATCATCAACTACGGGAACTCCGGGGGACCA
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Matches:
Conservative:
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FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/23,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/23,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/23,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/25,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 09/25,388
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR PRILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR APPLICATION NUMBER: 09/346,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR PRILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR APPLICATION NUMBER: 09/590,596
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US-09-796-753-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33, Application US/09796753 Publication No. US20030027998A1 GENERAL INFORMATION:
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VENTION: SECRETED PROTEINS AND USES THEREOF
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PRIOR APPLICATION NUMBER: 09/606,565
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR APPLICATION NUMBER: 09/605,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/65,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 33
LENGTH: 1563
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                                                                                                                      SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln
                                                                                                                                                                               CTGGTGAACCTGGATGGCGAGGTCATTGGCATCAACACGCTCAAGGTCACGGCTGGCATC
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SEQ ID NO 28
LENGTH: 1797
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/202,082
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 28
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NAME/KEY: misc feat
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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FILING DATE: 2001-05-04
APPLICATION NUMBER: 60/209,402
FILING DATE: 2000-06-01
APPLICATION NUMBER: 60/207,477
FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/205,803
FILING DATE: 2000-05-17
APPLICATION NUMBER: 60/203,566
FILING DATE: 2000-05-11
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HAFALIA, April J.A.; PATTERSON, Chandra
WALLA, Narinder K. KEARNEY, Limited M. Linger M. Linger M. Cannon M. 
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Application US/09818143
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SEQ ID NO 14
LENGTH: 2040
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APPLICANT: Volkmuth, Wayne
APPLICANT: Volkmuth, Wayne
APPLICANT: Volkmuth, Wayne
APPLICANT: WINGler Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
FILE REFERENCE: PB-0004 CIP
CURRENT APPLICATION UMBER: US/09/818,143
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 23
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ORGANISM: Homo sapiens
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LeuValAenLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIle
                                                                                                        SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro
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Pred. No.:
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APPLICANT: Song, Ho Yeong
APPLICANT: Su, Eric Wen
APPLICANT: Wang, He
TITLE OF INVENTION: Novel Secreted Proteins and Their Uses
FILE REFERENCE: X-13974
CURRENT APPLICATION NUMBER: US/10/381,820A
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/10381820A publication No. US20040142333A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2094
TYPE: DNA
ORGANISM: Homo :
FEATURE:
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LOCATION: (206)..(1564)
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             AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGln 89
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APPLICANT: Wyeth
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED I
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 5181
LENGTH: 2541
TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20050118625A1
                                                                                                                                                                                       GENERAL INFORMATION:
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               GluSerProLeuLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAla
                                                              ValLysValAsnGlyArgProLeuValAspSerSerGluLeuGl
                                                                                                                GlnGluValAlaProAsnSerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIle
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                                                                                                CAAGAGGTTGCGCCGAATTCACCTTCTCAGAGAGGCCGCCATCCAAGATGGTGACATCATC
                                                                                                                                                 GTGGATGAGCTGAAGGCCAGCAACCCGGACTTCCCCAGAGGTCAGCAGTGGAATTTATGTG
                                                                                                                                                                ValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrVal
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FILE REFERENCE: 31633 200357

CURRENT APPLICATION NUMBER: US/10/485,313A

CURRENT FILING DATE: 2004-01-30

PRIOR APPLICATION NUMBER: PCT/AU02/01010

PRIOR APPLICATION NUMBER: PR6707

PRIOR PILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

NUMBER: PATENTIAN DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PATENTIAN VERSION 3.1

SEQ ID NO 31

LENGTH: 2543

TYPE: DNA

ORGANISM: Homo sapiens

US-10-485-313A-31
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Query Match:
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US-10-485-313A-31
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APPLICANT: NIE, Guiying APPLICANT: SALAMONSEN, Lois Adrienne APPLICANT: SALAMONSEN, Lois Adrienne
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APPLICANT: HAMPTON, Anne Lorraine
APPLICANT: FINDLAY, John Kerr
TITLE OF INVENTION: Novel Serine Protease
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                                      ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGATCGCACCAGCCGTGGTCCACATAGAGCTCTTCCTGAGACACCCGCTGTTTGGCCGC
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                 GTGACAACGGGCATCGT
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No. US20050059002A1
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CURRENT APPLICATION NUMBER: U$/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/883,175
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR PELING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
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GENERAL INFORMATION:
APPLICANT: McCarthy,
TITLE OF INVENTION:
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US-09-796-753-31
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                                              OR FILING DATE: 1999-02-26
OR APPLICATION NUMBER: 60/122,458
OR APPLICATION NUMBER: 09/312,359
OR FILING DATE: 1999-05-14
OR APPLICATION NUMBER: 09/336,536
OR FILING DATE: 1999-06-18
OR APPLICATION NUMBER: 09/342,687
OR APPLICATION NUMBER: 09/342,687
OR FILING DATE: 1999-06-29
OR APPLICATION NUMBER: 09/345,464
OR FILING DATE: 1999-06-30
OR APPLICATION NUMBER: 09/365,164
OR APPLICATION NUMBER: 09/365,164
OR APPLICATION NUMBER: 09/399,723
OR APPLICATION NUMBER: 09/399,723
OR PILING DATE: 1999-09-20
OR APPLICATION NUMBER: 09/399,723
OR PILING DATE: 1999-09-20
OR APPLICATION NUMBER: 09/399,723
OR PILING DATE: 1999-09-20
APPLICATION NUMBER: 09/
FILING DATE: 1999-09-30
APPLICATION NUMBER: 09/
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VENTION: SECRETED PROTEINS AND USES THEREOF
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PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: 09/677,751

PRIOR FILING DATE: 2000-09-30

NUMBER OF SEQ ID NOS: 162

SEQ ID NO 31

LENGTH: 2576

TYPE: DNA

CRGANISM: Homo sapiens

US-09-796-753-31
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DB:
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Best Local Similarity:
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APPLICATION NUMBER: 09/0
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APPLICATION NUMBER: 09/630,334
FILING DATE: 2000-07-31
APPLICATION NUMBER: 09/606,565
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GTGACAACGGGCATCGTCAGCACTGCCCAGCGGGAGGGGAGCTGGGCCTCCGGGAC
                    ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp 169
                                                                                       AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr
                                                                                                                                                             AlaThrIleLysIleHisProLysLysLysLeuProValLeuLeuGlyHisSerAla
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                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/485,313A
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: PCT/AU02/01010
PRIOR FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: PR6707
PRIOR APPLICATION NUMBER: PR6707
PRIOR FILING DATE: 2001-07-30
VUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 2450
TYPE: DNA
ORGANISM: Mus musculus
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US-10-485-313A-26
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Publication No. US20050059002A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: SALAMONSEN,
APPLICANT: LI, Ying
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APPLICANT: FINDLAY, John Kerr
TITLE OF INVENTION: Novel Serine P
FILE REFERENCE: 31633-200357
                                                                                                                                       No.:
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RESULT 12
US-10-301-822-78
; Sequence 78, Application US/10301822
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; GENERAL INFORMATION:
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APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhang1
APPLICANT: Kamatkar, Shubhang1
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
APPLICANT: Burgart, Lawrence J.
APPLICANT: MORADAN, JOHN E.
APPLICANT: MORADAN, JOHN E.
APPLICANT: MOYEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILLE REFERENCE: MPMOI-029PZRNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 751
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                                               ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp 169
                                                                                                                  AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
                                                                                                                                                                   GCCACCATCAAGATCCATCCCAAGAAAAAGCTCCCTGTGTTGTTGCTGGGTCACTCGGCC
                                                                                                                                                                                       AlaThrIleLysIleHisProLysLysLysLeuProValLeuLeuLeuGlyHisSerAla
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Sequence 112, Application US/09764898
Patent No. US2002009673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PJZ01
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 112
LENGTH: 1868
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-898-112
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Query Match: DB:

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Percent Similarity: Best Local Similarity:

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  AATCTGGAGCCAGGCAGAGCCTGTCTTTCCCAAAGAAGCTGAAGTCTTCTTCTTCTTG
                    SerSerGluLeuGlnGluAlaValLeuThrGlu-----SerProLeuLeuLeu 315
                                                                       GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeu---ValAsp 299
                                                                                                       CAAGCACATKGDACCĊĊAGTGCAGĊĊAAGGCTGGTGCCATGAGGGCTGGTCACATGAAĠA 1026
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Sequence 32, Application US/10485313A

Publication No. US20050059002A1

GENERAL INFORMATION:

APPLICANT: NIE, GAIYING

APPLICANT: SALAWONSEN, Lois Adrienne

APPLICANT: LI, Ying

APPLICANT: HAMPTON, Anne Lorraine

APPLICANT: FINDLAY, John Kerr

TITLE OF INVENTION: NOVel Servine Protease

FILE REFERENCE: 31633-200357

CURRENT APPLICATION NUMBER: US/10/485,313A

CURRENT FILING DATE: 2004-01-30

PRIOR APPLICATION NUMBER: PCT/AU02/01010

PRIOR APPLICATION NUMBER: PCT/AU02/01010

PRIOR APPLICATION NUMBER: PS6707

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

INMBER OF SEQ ID NOS: 55

SOCTWARE: PATENTIN PATENT NUMBER: PS6707

PRIOR FILING DATE: 2001-07-30

INMBER OF SEQ ID NOS: 55

SOCTWARE: PATENTIN VERSION 3.1

SEQ ID NO 32

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Result
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## ALIGNMENTS

SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 AK035194 LOCUS REFERENCE REFERENCE DEFINITION JOURNAL MEDLINE JOURNAL MEDLINE TITLE TITLE AUTHORS AUTHORS PUBMED PUBMED Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., C., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., H. Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasl 2730 bp mRNA linear HTC 03-APR-2004 Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430098F20 product:hypothetical Serine proteases, trypsin family containing protein, full insert sequence. Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) protein, AK035194 Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) Mus musculus (house mouse)
Mus musculus HTC; CAP trapper. 11042159 20499374 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus AK035194.1 GI:26084456 .0349636 Enzymol. ., Harada,A., Kashiwagi,K., Carninci, P., new genes

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B 6 (bases 1 to 2730)

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Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 330-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
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Analysis of the mouse transcriptome of 60,770 full-length CNNs
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/db_xref="FANTOM_DB:9430098F20"
/db_xref="taxon:10090"
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plate: LLCM2410 row: i column: 18
High quality sequence stop: 605.
Location/Qualifiers
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BQ675502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 941)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domo sapiens (human)
                                                               GlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValValSer 75
                                                                                                                           ValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSerSer 55
                                             GGTTCTGGCTTCATCATGTCAGAGGCCGGCCTGATCATCACCAATGCCCACGTGGTGTCC
                                                                                                    GTCCACATAGAGCTCTTCCTGAGACACCCGCTGTTTGGCCGCAACGTGCCCCTGTCCAGC
                                                                                                                                                                         SerProArgTyrLysPheAsnPheIleAlaAspValValGluLysIleAlaProAlaVal
SerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAspSer 95
                                                                                                                                                          AGCCCGCGCTACAAGTTCAACTTCATTGCTGACGTGGAGAAGATCGCACCAGCCGTG
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                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:6256985"
/tissue_type="epidermoid carcinoma, cell line"
/lab_nost="PHIOB (phage-resistant)"
/clone_lib="NIH_MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis klt (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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56100663J1 FLP Homo sapiens
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Contact: Fu GK
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                                                                                                                                           6508454102
l: gfu@incyte.com
                                            /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clome lib="FLP"
/note="Vector: pDrive Clo
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182 AGCAACAGTGCTGCCCCGGGCAGGCAGCTCAAGGTGCAGCTACAGAATGGGGACTCC
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Genomics 84 (1), 205-210 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 810)
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Tetraodon nigroviridis full-length cDNA.

CR731516.

CR731516.1 GI;51229786

CR731516.1 retraodon nigroviridis.

Tetraodon nigroviridis

Tetraodon nigroviridis

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
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                                   LeuArgAspSerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSer
        GluPheGlnAspLysGlnIleLysAspTrpLysLysArgPheIleGlyIleArgMetArg
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/mol_type="mRNA"
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BQ880316.1 GI:22272324
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                             /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:6213159"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MCC_102"
/clone_lib="NIH MCC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoK1; cDNA made by oligo-dT priming.
Site_12: EcoK1; cDNA made by oligo-dT priming.
Site_13: EcoK1; cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
 1.39e-133
1191.00
92.81%
 Length:
Matches:
Conservative:
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Homo sapiens cDNA clone IMAGE:6213159
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Contact: Fu GK
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1 (bases 1 to 724)
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Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: gfu@incyte.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto,
Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
               pPheProGluValSerSerGlyIleTyrValGlnGluValAlaProAgnSerProSerGl
                                                                                                                                                           CATCAACACGCTCAAGGTCACGGCTGGCATCTCCTTTTGCCATCCCCTCAGACCGCCATCAC
                                                                                                                                                                                                                                                                                                                                   aIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaProGlyArgGlnGlnLeuLys-ValGlnLeuGlnAsnGlyAspSerTyrGluAlaTh
CTTCCCAGAGGTCAGCAGTGGAATTTATGTGCAAGAGGTTGCGCCGAATTCACCTTCTCA
                                                   CATACGGATGCGGACGATCACCAAGCCTGGTGGATGAGCTGAAGGCCAGCAACCCGGA
                                                                  YIleArgMetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAs
                                                                                                      ACGGTTCCTCACAGAGTTCCAAGACAAGCAGATCAAAGACTGGAAGAAGCGCTTCATCGG
                                                                                                                          rArgPheLeuThrGluPheGlnAspLysGlnIleLysAspTrpLysLysArgPheIleGl
                                                                                                                                                                              YIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleTh
                                                                                                                                                                                                             CATCATCAACTACGGGAACTCCGGGGGACCACTGGTGAACCTGGATGGCGAGGTCATTGG
                                                                                                                                                                                                                              aIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGl
                                                                                                                                                                                                                                                                  GCGGGAGGGCAGGGAGCTGGGCCTCCGGGACTCCGACATGGACTACATCCAGACGGATGC
                                                                                                                                                                                                                                                                                 nArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAl
                                                                                                                                                                                                                                                                                                                     CATCGGCAGTCCCTTCGCCCTACAGAACACAGTGACAACGGGCATCGTCAGCACTGCCCA
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sapiens
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/db_xref="taxon:9606"
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Contact: Richard G. Baumann
Bovine Functional Genomics Lab
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Plate: 34 row: P column: 04
Seq primer: CCTATTTAGGTGACACTATAGAAC
High quality sequence stop: 757.
Location/Qualifiers
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Baumann, R.G., Baldw
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                                                                                                                                       /tissue_type="Epithelial, Muscle"
/dev_stage="Inctating, Neonatal"
/lab_host="PHIOB TonA"
/clone_lib="BARC 8BOV"
/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSport6.1; Site_1: EcoRi; Normalized cow cDNA intestinal_library in pcMVSport6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 1/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
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                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV_34P04"
/sex="Female"
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   Contact : Feng Liang Email : fliang@lifetech.com URL http://fulllength.invitrogen.com/ InVitroGen Corporat Faraday Avenue
                                                 Bukaryota; Metazoa; Chordata; Craniata; Vert. Mammalia; Butheria; Primates; Catarrhini; Hol 1 (bass 1 to 1990)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Pull-length cDNA libraries and normalization Unpublished
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full-length cDNA clone
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Genoscope.

Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer: Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln
                                                                                                                                SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro
                                                                                                                                                                                           ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp
                                                                                                                                                                                                                                                          AspLeuArgProGlyGluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr
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/db_xref="taxon:9606"
/clone="CSODIO14YG06"
/tissue_type="placenta Cot 2
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Josef Lazar & Howard
College of Wisconsin
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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High quality sequence stop: 701.
Location/Qualifiers
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTTTGCCATCCCCTCAGACCGCATCACACGGTTCCTCACAGAGTTCCAAGACAAGCAG 1236
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/lab_host="DH10B TonA"

/clone lib="NIH MGC_252"

two days before RNA obtained from female overies animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification

(Tri_reagent method). cDNA was primed using oligo-dT primer: 5'-pGACTAGTTCTAGATCCCGAGCCCCC(T).25-3' and cloned into the EcoRV/Not1 sites of pExpress-1.

Size-selection >1.25bb resulted in an average insert size of 1.7kb. This primary library is not normalized (normalized library is not normalized by cormalized in a supersylate of the state of the
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Tissue was snap-frozen adn transferred in -70C. RNAse f
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/clone="IMAGE:7307090"
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798 bp mrangencourt 31536328 NIH MGC_269 Rattus IMAGE:7460898 5', mRNA sequence. CV106197.1 GI:51614770 EST.
                                                                  Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                 Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
Tissue Procurement: Dr. Josef Lazar,
College of Wisconsin
cDNA Library Preparation: Open Biosy
                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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      MetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAspPhe

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       Preparation: Open Biosystems
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us norvegicus cDNA clone
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Query Match:
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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IleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThr 219
                                                                IleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGly
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Location/Qualifiers
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/note="Qrgan: placenta; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NotI; Tissue was collected from two pooled
placentas from the 21st day of pregnancy. 1st strand cDNA
was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was cloned into the Not I and EcoRV
sites of pExpress-1. Library was size-selected for >1.25
kb fragments for an average insert size of 2.05 kb. A
normalized version of this library is also available
(NIH_MGC_270). Library was constructed by Open Biosystems
(Huntsvile, AL). Note: this is a Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:7460898"
/tissue_type="whole placenta,
/lab_host="DH10B TonA"
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                                                                      US-10-617-443B-2 (1-334)
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Kurphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 973)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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GGCAGGAAGATCCCAACAGTTTGCGCCATAAATATAACTTTATCGCGGACGTGGTGGAG
                GlyLeuHisGlnLeuSerSerProArgTyrLysPheAsnPheIleAlaAspValValGlu
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                          gene="PRSS11"
                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                         locus_tag="HCM2427"
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RESULT 12
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CR590731
CR590731.1 GI:50471538
HTC; CNSLT_CDNA.
                                                    CR590731
full-length cDNA
                                           (human)
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                                                                                                                             ACAGTGATTĊĊĊĠAAGAAATT
                                                                                                                                                SerIleAlaProGluValVal 333
                                                                                                                                                                                    AspIleIleValLysValAsnGlyArgProLeuValAspSerSerGluLeuGlnGluAla
                                                                                                                                                                                                                                                                                                  GCGTATATAATTGAAGTAATTCCTGATACCCCAGCAGAAGCTGGTCGTCGAAGGAAAAC
                                                                                                                                                                                                                                                                                                                          IleTyrValGlnGluValAlaProAsnSerProSerGlnArgGlyGlyIleGlnAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                TCCTTTGCAATCCCATCTGATAAGATTAAAAAGTTCCTCACGGAGTCCCATGACCGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln
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                                                                                                                                                                                                                                              GACGTCATAATCAGCATCAATGGACAGTCCGTGGTCTCCGCCAATGATGTCAGCGACGTC
                                                           1655 bp mRNA linear clone CS0DE011YH20 of Placenta of
                                                                                                                                964
                                                                          mRNA
                                                                       linear
                                                             Homo
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                                                             sapiens
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was primed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1655)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                        4 AlaLeuProAlaSerAlaGlyLeuHisGlnLeuSerSerProArgTyrLysPheAsnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact : Feng Liang Email : fliang@lifetech.
http://fulllength.invitrogen.com/ InVitroGen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Faraday Avenue
                                                                                                                                                                                                                                                                                         CACCGGGTCAAAGTTGAGCTGAAGAACGGTGCCACTTACGAAGCCAAAATCAAGGATGTG
                                                                                                                                                                                                                                                    AlaGlyLeuIleIleThrAsnAlaHisValValSerSerAsnSerAlaAlaProGlyArg
                                                                                                                                                                                                                                                                                                                                                  ### ATCGCGGACGTGGTGGAGAAGATCGCCCTGCCGTGGTTCATATCGAATTGTTTCGCAAG
                                                                                                                                                                                                                                                                                                                                                                 | IleAlaAspValValGluLysIleAlaProAlaValValHisIleGluLeuPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                          GCGGAGCCTGCGGCCAAGGGCAG-GAAGATCCCAACAGTTTGCGCCATAAATATATAACTTT
                                                                                   LeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValValAlaIleGlySerPro
                                                                                                                                      AspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLysLeuProValLeu
                                                                                                                                                                                              GlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIle 103
                                                                                                                                                                                                                                     GATGGACTGATCGTGACAAATGCCCACGTGGTGACCAAC------AAG
                    PheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArgGluGlyArg
                                                                                                                       GATGAGAAAGCAGACATCGCACTCAAAAATTGACCACCAGGGCAAGCTGCCTGTCCTG
       CTGCTTGGCCGCTCCTCAGAGCTGCGGCCGGGAGAGTTCGTGGTCGCCATCGGAAGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="CS0DE011YH20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.83e-114
1034.50
80.18%
61.86%
61.61%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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MEDLINE
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                                                                                          Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buctow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsteh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheet, T.E., Brownstein, M.J., Usdin, T.B., Toshiyaki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1911 bp mRNA linear HTC 19-NOV-20
Homo sapiens protease, serine, 11 (IGF binding), mRNA (cDNA clone
IMAGE:4177882), containing frame-shift errors.
BC011352
BC011352.1 GI:15030191
                                                  human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCTGGGGCTCCGCAACTCAGACATGGACTACATCCAGACCGACGCCATCATCAACTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGGTCTCAAGGAAAACGACGTCATAATCAGCATCAATGGACAGTCCGTGGTCTCCGCC
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium of DNA Sequencing by: Baylor College of Medicine Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.N., Gibbs, R.A.
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., I
Kowie, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M.,
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/clone_lib="NCI_CGAP_Brn67"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4177882"
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1931)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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                                                                                                                   Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                     HTC; CNSLT_cDNA.
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                                                                                                                                                                                                                                                                                                                                                                   gargagahagcagacarcgcacrcarcahaharrgaccaccagggcahagcrgccrgrccrg
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                                                                                                                                                                                                                                                                                                                                                                                                                      CACCGGGTCÁÁAGTTGAGCTGAAGÁACGGTGCCACTTÁCGAAGCCAAAÁTCÁAGGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnGlnLeuLysValGlnLeuGlnAanGlyAapSerTyrGluAlaThrIleLysAspIle 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaGlyLeuIleIleThrAsnAlaHisValValSerSerAsnSerAlaAlaProGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisProLeuPheGlyArgAsnValProLeuSerSerGlySerGlyPheIleMetSerGlu
                                                                                                                                                                                                                            LeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValValAlaIleGlySerPro
                                                                                                                          LysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThr
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                                                                    GluPheGlnAspLysGlnIleLysAsp-----
                                                                                                       AAAGTGACAGCTGGAATCTCCTTTGCAATCCCATCTGATAAAGATTAAAAAGTTCCTCACG
                                                                                                                                                         GGAAACTCGGGAGGCCCGTTAGTAAACCTGGACGGTGAAGTGATTGGAATTAACACTTTG
                                                                                                                                                                      GAGTCCCATGACCGACAGGCCAAAGGAAAAGCCATCACCAAGAAGAAGTATATTGGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol type="mRNA"
/db_xref="raxon:9606"
/clone="CSODIO75YN06"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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REFERENCE
AUTHORS
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CR624458
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24 IleAlaAspValValGluLysIleAlaProAlaValValHisIleGluLeuPheLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web: www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five end enriched, double-strand cDNA was digested with Not I and into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Li was normalized. Library was constructed by Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 1951)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR624458.1 GI:50505265
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1951 bp mRNA linear HTC 21-JUL-2004
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                    GCGGAGCCTGCGGCCAAGGGCAG-GAAGATCCCCAACAGTTTGCGCCCATAAATATAACTTT
                                                           AlaLeuProAlaSerAlaGlyLeuHisGlnLeuSerSerProArgTyrLysPheAsnPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnAspAspLeuLeuPheSerIleAlaProGluValVal 333
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                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODKO12YA20"
/tissue_type="HeLa cells C
/plasmid="pCMVSPORT_6"
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                                                                                         SerGluLeuGlnGluAlaValLeuThrGluSerProLeuLeuGluValArgArgGly
                                                                                                                                               GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer
                                                                                                                                                                                                                                                                                                                GAGTCCCATGACCGACAGGCCAAAGGAAAAGCCATCACCAAGAAGAAGTATATTGGTATC
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                           AsnAspAspLeuLeuPheSerIleAlaProGluValVal 333
                                                             AATGATGTCAGCGACGTCATTAAAAGGGAAAĞCACCCTGAACATGGTGGTCCGCAĞGGGT
                                                                                                                                                                                    CCAGACGTGATCTCAGGAGCGTATATAATTGAAGTAATTCCTGATACCCCAGCAGAAGCT
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AATGAAGATATCATGATCACAGTGATTCCCGAAGAAATT 1446
                                                                                                                          GGTGGTCTCAAGGAAAACGACGTCATAATCAGCATCAATGGACAGTCCGTGGTCTCCGCC
                                                                                                                                                                                                                                                     CGAATGATGTCACTCACGTCCAGCAAAGCCAAAGAGCTGAAGGACCGGCACCGGGACTTC
                                                                                                                                                                                                                                                                                 ArgMetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAspPhe
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5 UI-R-AC1-3

3 UI-R-AC1-3

3 UI-R-BC1-3

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3 UI-R-BC1-3

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CV029025 7690 Full CV0259057 170004706				A1553578 vw42c02.x BE860202 UI-M-A00- CN259060 170006000	

## ALIGNMENTS

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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                  clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG120009.1 GI:16649174
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                                                                                                                                                                                                                                                                                                                                                           Sequencing: -21M13
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R.Site 1
R.Site 2
                                                                                                                                  /organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="PTB-128K01.F"

/sex="male"
                                                                                     /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Location/Qualifiers
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BQ574834
BQ574834.1 GI:21478151
EST.
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The following repetitive elements were found in this cDNA sequence: 176-463, >ALU (matched compliment)
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
/note = "Organ: Left Pelvis; Vector: PT7T3-Pac (Pote)
/note = "Organ: Left
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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0; Mismatches
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RESULT 4
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project
This clone (DKFZD313M0539) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp313M0539 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bahr,A., Lauber,J., Mewes,H.W. Fobo,G., Han,M. and Wiemann,S. The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-JUL-2004) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nomou4/41 2534 bp mRNA linear HTC 03-AUG-2004
Homo sapiens mRNA; cDNA DKFZp313M0539 (from clone DKFZp313M0539).
AL833428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2534)
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                                            h 2.3%; Scy
Similarity 100.0%; P:
24; Conservative 0;
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TGAGGCCACACAGCTAGAAAGCAG 141
                                                                                                                                                                                                   SDTSVIQFYPSKFVLITDILDTFGKLVYERIFSMCVDSRSVLPDHFSPENANDTAKET
CLNWFFKIASIRELIPRFYVEASILKCNKFLSKTGISECLPRLTCMIRGIGDPLVSVY
ARAYLCRVGMEVAPHLKETLNKNFFDFLLTFKQIHGDTVQNQLVVQGVELPSYLPLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="heart"
/clone_lib="313 (synonym: hlcc2). Vector pTriplEx2; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                        /trānslation="mavfpwhsrnrnykabfascrleavplefgdyhplkpitvtesk
TKKVNRKGSTSSTSSSSSSVVDPLSSVLDGTDPLSMfaatadpaalaaamdSSRRKR
DRDDNSVVGSDFEPWTNKRGEILaryttteklsinlfmGSEKGKaGtatlamsekvrt
                                                                                                                                                                              PAMDWIFQCISYHAPE"
                                                                                                                                                                                                                                                                             RLEELDDSEEGSQKELLNLTQQDYVNRIEELNQSLKDAWASDQKVKALKIVIQCSKLL
                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
/protein_id="CAH10399.1"
/db_xref="GI:50949538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="DKFZp313M0539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="DKFZp313M0539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"esophageal cancer associated protein, C-terminus runcated, not fully spliced"
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'db_xref="taxon:9606"
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/mol_type="mRNA"
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                                               Score 24; DB; Pred. No. 1. 0; Mismatches
                                                                                            DB 3;
                                                  0,
                                                                                               Length 2534;
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TGAGGCCACACAGCTAGAAAGCAG 1491

BG548488

728 bp

mRNA

linear

EST 04-APR-2001

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DEFINITION

602575077F1 NIH_MGC_77

Homo sapiens cDNA clone IMAGE: 4703322 5',

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491
1 (bases 1 to 125)

1 (bases 1 to 125)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chiko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA Sequence and construction of a gene index for cattle
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                          Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                               BM481069 125 bp mRNA linear
532861 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
BM481069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consort http://image.llnl.gov plate: LLCM1541 row: i column: 19 High quality sequence stop: 695. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            BM481069.1
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Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCCAGGCCCAGCCGAACCCCT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCCAGGCCCAGCCGAACCCCT 161
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/clone="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 77"
/clone lib="NIH MGC 77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 2:
Sfil (ggccgcttggcc); Site 2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor sequence:
S'-CACGCCCATTATGGCC-3' and 3' adaptor sequence:
S'-ATTCTAGAGGCGGCCGACATG-dT(30) BN-3' (where B = A;
S'-ATTCTAGAGGCCGACGGCGCCGACATG-dT(30) BN-3' (where B = A;
S'-ATTCTAGAGGCCGACGGCGCCGACATG-dT(30) BN-3' (where B = A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                 National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: B0281 row: B column: 08 Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H. Construction of long-transcript enriched cDNA libraries submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs by a universal PCR and submicrogram amounts of total RNAs 
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498 bp mRNA linear EST 11-JUN-2003
B0281B08-5 NIA Mouse Embryonic Germ Cell cDNA Library (Long) Mus
musculus cDNA clone NIA:B0281B08 IMAGE:30111187 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 498)
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CD547336
CD547336.1 GI:31595071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21429098
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Single pass sequencing. Bases call
v0.980904.e. Vector identified by
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PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11544199
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BACKWARD: GTTTTCCCAGTCACGACG
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                  Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9913"
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/lab_host="DH10B"
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Laboratory of Genetics
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, t
Email: cdna@lgun.grc.nia.nih.gov
niato. Rn374 row: A column: 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                      505 bp mRNA linear B0374A09-5 NIA Mouse E9.5 Whole Embryo CDNA Library musculus CDNA clone NIA:B0374A09 IMAGE:30436136 5', CD554299
                                                                                                                                                                                                                        Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplif:
                                                                                                                        Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 505)
                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                              11544199
                                                                                                                                                                                   Genome Res. 11 (9), 1553-1558 (2001)
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/notes "Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sall;
Site 2: Noti, Mouse cDNA project by the Laboratory of
GeneTics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were obtained from Dr.Mark G. Carter (NIH/NIA-IRP).
EG cells were cultured at 37. C, 5% CO2 in DMEM
supplemented with 15% ES cell-qualified FBS, 0.1mM
non-essential amino acids, 2 mM glutamine,
penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM
beta-mercaptoethanol, and 10000000 units of LIF per liter.
Double-stranded cDNAs: were synthesized with an Oligo(dT)
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/db_xref="taxon:10090"
/clone="NIA:B0281B08 IMAGE:30111187"
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/lab_host="DH10B"
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REFERENCE AUTHORS

TITLE

COMMENT

JOURNAL MEDLINE

KEYWORDS SOURCE ORGANISM

/ERSION ACCESSION RESULT 7 CD554299/c

DEFINITION

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Matches Query Match

22;

Local

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462 AGTCCCATTTTCAGATGAGGA 441
Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                            UI-M-FY0-cfk-p-20-0-UI.rl NIH
IMAGE:6850917 5', mRNA sequenc
                                                             Email: cgapbs-r@mail.nih.gov
                                                                             Contact: Robert Strausberg,
                                                                                                         NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 744)
                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                 CB528031
CB528031.1
                                                                                                                                                                                                                                                                                            CB528031
                                                                                              Unpublished (1999)
                                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIA Mouse E9.5 Whole Embryo cDNA Library
(Long)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="niaEST:B0374A09-5"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                 GI:29361504
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                                                                                                                                                                                                                                                              mRNA sequence.
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Pred. No.
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                               University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346
                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 922)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602023960F1 NCI_CGAP_Li9
                                                                                           Plate: LLAM9436 row: h column: 15 High quality sequence stop: 622.
                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF233030.1 GI:11143008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone Distribution: Distribution information can be found http://genome.uiowa.edu/distribution/mousefl.html This clone was contributed by the Brain Molecular Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: pYX-5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (house mouse)
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//dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH108 [T1 phage resistant)"
/clone lib="NIH BMAP FYO"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library teg
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                       Location/Qualifiers
                      organism="Mus musculus"
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100.0%; Mismatches
_type="mRNA"
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Curr. Bi
22335534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1706)

1 (bases 1 to 1706)

1 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs
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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Simon. Hubbard@umist.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PO Box 88, Manchester, Tel: 01612008930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. 12 (22), 1965-1969
                                     /note="Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and Ligate in double stranded adaptor containing BsgI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4159166"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BamHI sites [5/ggccgcgtgcagccccggatccgaaaaaaag]
[5/aattctttttttcggatccggggctgcacgc]"
                                                                                                                                                                                                                                                         /dev_
                                                                                                                                                                                                                                                                            cartilage"
                                                                                                                                                                                       /clone_lib="CSEQRBL03"
/note="Vector: pBluesc
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                lab host="DH108"
                                                                                                                                                                                                                                                                                                tissue_type="Chondrocytes isolated from growth plate
                                                                                                                                                                                                                                                                                                                        sex="Male and
                                                                                                                                                                                                                                                                                                                                                                                                    organism="Gallus gallus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                         clone="ChEST175g8"
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                                                                                                                                                                                                                                                                                                                                                                                 strain="Layer and broiler"
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                                                                                                                                                                                                                                                    _stage="adult"
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s cDNA clone ChEST175g8
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L Nature 420, 563-573 (2002)

E 6 (Dases 1 to 193)

E 6 (Dases 1 to 193)

S Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Alachi, J., Alzawa, K., Akahira, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K., Furuno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K., Hiraoka, T., Kori, F., Imotani, K., Ishii, Y., Konno, H., Kouda, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Sajahi, A., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
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Mus musculus (house mouse)
Mus musculus
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HTC; CAP trapper.
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in R Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed
                                                                                                       Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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URL:http://fantom.gsc.riken.jp/.
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Please visit our web site for further details
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Shibata,K., Itoh,M., Aizawa,K.,
Konno,H., Akiyama,J., Nishi,K.,
Sumi,N., Ishii,Y., Nakamura,S.,
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99279253
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match=822)"
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dev_stage="12 days embryo"
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                                                                                                                                                                                                                                                                                                                                         Metazoa;
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ency full-length cDNA cloning
ol. 303, 19-44 (1999)
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Rodentia;
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Sciurognathi; Muridae;
   Nagaoka,S., Sasaki,N., C
Kitsunai,T., Tashiro,H.,
Hazama,M., Nishine,T., H
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Encyclopedia Próject of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax.81-45-503-9216)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                        'note="unknown EST
                                                                                                                                                                                                                                                                                                                           dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                               tissue type="aorta and vein" clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="A530040I21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="FANTOM_DB:A530040I21"
'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _type="mRNA"
                                                                                                                               2.1%; Score 22;
100.0%; Pred. No.
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                                                                                                         <u>,</u>
604
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                                                                                                         Mismatches
                                                                                                                                                                                                                                                                        (GB|BI251132, evidence: BLASTN,
                                                                                                                                  DB 3;
17;
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                                                                                                         Indels
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                                                                                                      Gaps
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CR516621
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1 (bases 1 to 207)
Henrich, J., Hermanns, J., Kranz, H., L
Schuette, D., Weindel, M., Heil, O., Eb
Radelof, U., Schneider, D. and Korn, B.
Mouse ArrayTAG cDNA
Unpublished (2004)
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fue
                                                                                                                                                                                                                                                                                                                                                                                                                                             903
                                                                                                                                                                                                                                                                                                                                                                                                          48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                           CR516621 207 bp CR516621 Mouse pBluescript Lion LIONp462B0815 3', mRNA sequence
                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                       CR516621.1
                                                                                                                                                                                                                                                          LIONp462B0815
CR516621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11327 row: e column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 204)
NIH-MGC http://mgc.nci.nih.gov/
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BI329065.1
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602980483F1 NCI_CGAP_Li9 Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc. (LLNL) CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGGGCTGAGGCTGGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:5133309"
/clone="IMAGE:5133309"
/clone=lib="NGICAP_Li9"
/clone=lib="NCI_CGAP_Li9"
/clone="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="FVB/N"
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Pred. No.
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                                                                                                                                                                                                                                                                                                Mus musculus
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57;
     fuer
                                                                                          Loebbert,R., Schlueter,T.,
3bert,L., Neubert,P., Peters,M.
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BB200500/c
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http://www.rzpd.de/cgi-
http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi/response?libNo=462 Contact: Inge Arlart
bin/products/showLib.pl.cgi/response?libNo=462 Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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Email: www.rzpd.de
RZPD, LIONp462B0815.
                                                                                                                                                                                                                                                                                                             Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Kusakabe, M., Matsuyama, T., Saito, H., Sakai, C., Sato, K., Kusakabe, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigamoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Shiraki, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Wattahiki, A., Yatohashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Wattahiki, A., Yoshiki, A., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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BB200500.1 GI:8865453
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                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
                                                                                                                                                                                                                                    RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; mur
1 (bases 1 to 238)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                            Carninci
                                                                                 Fax: 81-45-503-9216
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genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
ci.p., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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/db xref="taxon:10090"
/clone="LION9462B0815"
/lab host="DH10B"
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Search completed: June 29, 2005, 21:07:12 Job time : 4086 secs

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ilarity 100.0%;
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/dev_stage="0 day neonate"
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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RESU US-0 ; Se ; Pa ; Pa ; T T	Que Bes Mat Qy	C		000 00
SSULT 2 3-09-949-016-12591, Appl Sequence 12591, Appl Patent NO. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, TITLE OF INVENTION: FILE REFERENCE: CLIO CURRENT APPLICATION CURRENT FILING DATE	ry M t Lo ches	URREN URREN RIOR RIOR RIOR RIOR RIOR RIOR OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD OFTWD	SSULT 1  -09-949-016-13413/c S-09-949-016-13413, Applipatent No. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: CLOO	22250000000000000000000000000000000000
949-016-12591 949-016-12591, Application US/09945 ence 12591, Application US/09945 nt No. 6812339 RAL INFORMATION: LICANT: VENTER, J. Craig et al. LICANT: VENTER, J. Craig et al. LE OF INVENTION: WITH HUMAN DIS E REFERENCE: CL001107 RENT APPLICATION NUMBER: US/09/9 RENT FILING DATE: 2000-04-14	9 1 22 1	IT FILING DATE: APPLICATION NUM FILING DATE: 20 APPLICATION NUM FILING DATE: 20 APPLICATION NUM FILING DATE: 20 OF SEQ ID NOS: RE: Fast SEQ for NO 13413 H: 116652 DNA IISM: Human RRE: RB: Tast SEQ for IISM: GRE: IISM: Human RB: IISM: Human IISM: Human IISM: His 16652 DNA IISM: Human IISM: Human IISM: Human IISM: Human IISM: Human IISM: His 16652 DNA IISM: Human II	016-13413/c 13413, Appl 0. 6812339 INFORMATION: WIT: VENTIEN: FINVENTION: FINVENTION: FERENCE: CLO	
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-09
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 15871
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12591
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Best Local Similarity
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Patent No. 6812339
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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FEATURE:
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OTHER INFORMATION: n = A,T,C or
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FEATURE:
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LOCATION: (1)...(65744)
OTHER INFORMATION: n = A,T,C
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RESULT 6 US-09-949-016-14548

Sequence 14548, Appl Patent No. 6812339 GENERAL INFORMATION:

Application US/09949016

APPLICANT: VENTER, J. Craig et al.

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1).T. (818128)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-14547
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; NAME/KEY: misc feature
; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14546
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 14547
LENGTH: 818128
TYPE: DNA
                                                                                                                                                              Matches
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Patent No. 6812339
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-04-14
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116875 AGGCCACACAGCTAGAAAGCA 116895
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                                                      120 AGGCCACACAGCTAGAAAGCA 140
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                                                                                                                                                          21;
                                                                                                                                                                                                    Similarity
                                                                                                                                                  2.0%; Score 21; DB 4 ilarity 100.0%; Pred. No. 2.9; Conservative 0; Mismatches
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RESULT 8
US-09-949-016-14550
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: LOCATION: (1)...(818128)

: OTHER INFORMATION: n = A

US-09-949-016-14548
                                                                                                                                                            Matches
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Patent No. 6812339
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Best Local Similarity
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SEQ ID NO 14548
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207712
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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PRIOR APPLICATION NUMBER: 60/241,755
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                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
FEATURE:
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CURRENT FILING DATE: 2000-04-14
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ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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                                                                                                                                                                              Local Similarity
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                                                                                          AGGCCACACAGCTAGAAAGCA 116895
                                                                                                                                                            Conservative
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100.0%; Pr
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Pred. No.
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Pred. No.
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; LOCATION: (1) ... (818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14551
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SEQ ID NO 14551
LENGTH: 818128
                                                                            Matches
                                                                                        Query Match 2.0%;
Best Local Similarity 100.0%;
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APPLICANT: VENTER, J.
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LENGTH: 81812
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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SOFTWARE: FastSEQ for
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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LOCATION: (1)...(818128)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                    TYPE: DNA
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116875 AGGCCACACAGCTAGAAAGCA 116895
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                                    120 AGGCCACACAGCTAGAAAGCA 140
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                                                                          Conservative
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                                                                                        Score 21; ; Pred. No.
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Pred. No.
                                                                          Mismatches
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2.9;
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OF DETECTION AND USES THEREOF
                                                                                                          Length 818128;
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RESULT 10 US-09-949-016-14552

Sequence 14552, Apparent No. 681233

Application US/09949016

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116875 AGGCCACACAGCTAGAAAGCA 116895

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RESULT 11
US-09-949-016-14553
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; LOCATION: (1)...(818128)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-14552
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION UNMEER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14553
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14
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PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                             Matches
                                                                                            Query Match
                                                                                                                                    FEATURE:
NAME/KEY: misc feature
LOCATION: (1).T. (818128)
OTHER INFORMATION: n = A,T,C
-09-949-016-14553
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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ilarity 100.0%;
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Pred. No. 2.9;
0; Mismatches
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PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14555
LENGTH: 818128
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NAME/KEY: misc_feature

LOCATION: (1)...(818128)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14554
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                                                                                   ; NAME/KEY: misc_feature
; LOCATION: (1)...(818128)
. OTHER INFORMATION: n = A,T,C
US-09-949-016-14555
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION UNMEER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14555, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
FULB REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Best Local
Matches
                                       Query Match
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Similarity 100.0%; Pred. No.
  Similarity
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                           2.0%; Score 21; DB 4;
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; CRGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1):..(818128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14556
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US-09-949-016-14556
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Best Local Similarity
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Patent No. 6812339
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PEATURE:

NAME/KRY: misc feature

LOCATION: (1)...(818128)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CL001307
                                                                                                                        ORGANISM: Human
                                                                                                                                                LENGTH: 818128
TYPE: DNA
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Query Match 2.0%; Score 21; DB 4; Length 818128;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 120 AGGCCACACACGCTAGAAAGCA 140
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Search completed: June 29, 2005, 21:11:05 Job time : 234 secs

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116875 AGGCCACACAGCTAGAAAGCA 116895

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd

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Aaf21695 Human bre
Add47518 Human gen
Add47514 Human gen
Add47514 Human gen
Add37665 Human can
Adjill359 PCR prime
Add99925 Kidney di
Ab19990 Human sec
Add97121 Human tum
Ab236074 Human sec
Add87103 Human pro
Add90254 Hermansky
Acf62741 Cancer ba
Adb20856 MRP1 base
Adb20856 MRP1 base
Adb20856 Human MDR
Add511361 PCR prime
Adb99119 Human MDR
Add511361 PCR prime
Adb57333 Human int
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19	19	19	19	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20
1.8	1.8	1.8	1.8	1.91	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9
290	254	251	89	117962	94531	94529	94529	87761	79860	55875	26000	26000	15720	15720	15720	15720	15720	15720	15720	15720	15720	15720	3294	836
6 ABV95882	7 ADS65486	12 ADM72179	3 AAC12336	8 AAD54480	9 ADA66370	10 ADB72824	9 ADA03086	11 ADL27164	11 ACN44122	12 ADQ59503	13 ADR82648	13 ADR86701	13 ADQ80264	12 ADQ29628	11 ADP88236	11 ADP88237	10 AAD62742	10 AAD63141	8 ACD13431	8 ABZ33690	6 ABL62358	4 AAI29504	4 AAH57441	2 AAQ12218
Abv95882 Human pan	Ads65486 Corn seed	Adm72179 Human NTR	Aac12336 Human sec	Aad54480 Human CIP	Ada66370 Human hCG	Adb72824 Human hCG	Ada03086 Human hCG	Adl27164 Human gen	Acn44122 Human gen	Adq59503 Human can	Adr82648 Human Eph	Adr86701 Human Eph	Adq80264 Intestina	Adq29628 Human col	Adp88236 Colon can	Adp88237 Colon can	Aad62742 Human muc	Aad63141 Human muc	Acd13431 Human DNA	Abz33690 Human col	Abl62358 Colon ade	Aai29504 C899P det	Aah57441 Human int	Aaq12218 SMUC-41 i

## ALIGNMENTS

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RESULT 1
ADJ11355
ID 11355
ID 120-M
XX ADJ1
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                                                                                                                                                                                                                                    WPI; 2004-081723/08.
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(QLJJ/) QL J.
(CHEN/) CHEN C.
(ANDR/) ANDRADE-GORDON P.
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                                                                                                                                                                                                                                                                                                                    Andrade-Gordon
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New isolated S2 serine protease nucleic acids and polypeptides, useful for diagnosing and/or treating diseases with aberrant expression or activity the S2 serine protease, such as osteoarthritis, stress and

apoptotic disorders

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3006 BP; 615 A; 918 C; 911 G; 562
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Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepaatotropic; antidiabetic;

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                                                                                                                                                                                                                                                                                                                    New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic;
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kit to perform the method, an array, a member of identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal risery of
                                                                                                                 claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and in the compression of the compre
                                                                                                                                                                                                                                                The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antifungal; antiparasitic and cardiant activity. The polymucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular diseases such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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New composition comprising two or more isolated polypeptides, preparing a medicament for treating pain in an animal.

useful

for

Example 1; Page; 1017pp;

invention discloses a composition comprising two

or more isolated

rat

English

claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and the comprising the vector.

or human po derivative

polynucleotides or a pove or allelic variation

a polynucleotide which represents a fragment, tion of the nucleic acid sequence. Also

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cc which is differentially regulated in an animal subjected to pain and a ckit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence cc that is differentially expressed in neuronal tissue of a first animal conjuncted to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the collection, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating composition, a method for identifying a compound useful in treating composition and a pharmaceutical composition composition composition or the compound that composition composition of the polypeptides or their antibodies. The polynucleotide or the compound that condulates its activity is useful for preparing a medicament for treating condulates its activity is useful for preparing a medicament for treating conjury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene condulates its activity is useful for preparing a medicament for treating conjury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene constitution of the specification) which encodes one of the polypeptides of the invention contained in electronic form directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                              14-FEB-2003; 2003US-00367094.

14-MAR-2003; 2003US-0038838.

15-APR-2003; 2003US-00417375.

13-JUN-2003; 2003US-00461862.

15-SEP-2003; 2003US-00663431.

15-DEC-2003; 2003US-00737318.
                                                                   Morrie DW,
                                                                                                                                                                                                                                                    17-FEB-2004;
                                                                                                                                                                                                                                                                                     02-SEP-2004.
                                                                                                                                                                                                                                                                                                                      WO2004074320-A2
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cancer-associated genomic DNA HD13-070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABD32665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD32665 standard; DNA; 112453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4558 BP; 1030 A; 1062 C; 1303 G; 1163 T; 0 U;
                                                                                                  (SAGR-)
                                                                                                                                                                                                                                                                                                                                                                                     leukaemia; lymphoma; CAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POCHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         772 GGTCCAGTGAGGGGGGGTGAGGA 793
                                                                                                  SAGRES DISCOVERY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTCCAGTGAGGGGGGGTGAGGA 4166
                                                                                                                                                                                                                                                                                                                                                                                                  cancer-associated protein; gene; cytostatic; cancer;
                                                                   Morris DW,
                                                                                                                                                                                                                                                    2004WO-US004730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                   Malandro
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Pred. No.
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                                                                   S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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claim 16;
                                                                                                                                                                                               New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                                                                                                                                                                                     seqid 209; 310pp; English.
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Coin the specification, or its complement. The nucleic acids encode cancercassociated proteins. Also included are an expression vector comprising
the isolated nucleic acid or expression vector, a microarray for detecting
crecombinant nucleic acid or expression vector, a microarray for detecting
cc comprising at least 10 contiguous nucleotides of any of the abovecc mentioned nucleotide sequences, an isolated polypeptide (encoded within
cc an open reading frame of a CA sequence selected from any of the 95
cc polynucleotide sequences as mentioned in the specification, or its
cc omplement), an isolated antibody, (or its antigen binding fragment) that
binds to the above polypeptide, a hybridoma that produces the above
cc antibody and a pharmaceutical excipient, a kit for detecting cancer
cc cells (comprising the antibody cited above, methods for disgnosing cancer
cc individual, a method for inhibiting growth of cancer cells in an
cc individual, a method for thibiting growth of cancer cells in an
cc individual, an electronic library comprising the above
polynucleotide or polypeptide (or their fragments), methods of screening
cc the activity of a CA protein (CAP), methods for detecting cancer
cc associated with expression of a polypeptide in a test cell sample, a
cc method for treating cancers and a method for inhibiting the expression of
cd diagnosing, preventing and treating cancers, sepecially lymphoma and
cc ancer. The present sequence is a human CAP genomic sequence. Note: The
sequence data for this patent did not form part of the printed
cancer from wino intrombinal shad not agent for mat directly from wipo at ftp.wipo.int/pub/published_pct_sequences The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancer-

Sequence 112453 BP; 28299 A; 24810 C; 27274 G; 32070 T; 0 U; O Other,

밁 S Matches Query Match Best Local 33503 CTGTCTGAGGCCACACAGCTAG 33482 113 22; Similarity CTGTCTGAGGCCACACAGCTAG Conservative 100.0%; F1 2.1%; Score 22; 100.0%; Pred. No. 134 Mismatches 4 DB 13; .6 0 Length 112453; 0 Gaps 0

## RESULT 6 ADJ11359 ADJ11359 standard; DNA; 34 BP

PCR primer used to construct the human PRSS11-L expression vector SeqID5. 20-MAY-2004 ADJ11359;

(first entry)

human; PRSS11-L; PCR; ss; S2 serine protease; S2/HtrA; cellular physiology; apoptosis; gene therapy; osteoarthritis; stress; apoptotic; hysiology; apoptosis; gene to osteopathic; antiarthritic;

Synthetic Homo sapiens

08-JAN-2004. US2004005659-A1

03-JUL-2002; 2002US-00189099.

0

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RESULT 7
ADG99925/c
ID ADG999
XX
ADG99
XX
A
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel isolated nucleic acid molecule identified as PRSS11-L that encodes an S2 serine protease. Specifically, it refers to members of the S2/HtrA serine protease family, such that it plays a role in cellular physiology and apoptosis. The present invention provides agonists, antagonists, antibodies and recombinant expression vectors useful in methods of treatment, or detection and diagnosis of diseases associated with the aberrant expression or activity of the S2 serine protease, PRSS11-L. Accordingly, compositions described herein can be used via gene therapy routes to treat osteoarthritis, stress and apoptotic disorders. As such, they exhibit osteopathic, antiarthritic and tranquiliser activities. This oligonucleotide sequence is a PCR primer used to construct the recombinant expression vector for human PRSS11-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kidney disease;
diabetic renopa
Kidney disease-associated genes expressed in proximal tubule, applicable
                                                                                                                                                                                                               24-APR-2002; 2002JP-00122253
                                                                                                                                                                                                                                                             23-APR-2003; 2003WO-JP005137
                                                                                                                                                                                                                                                                                                                         06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                          WO2003091427-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kidney disease-associated gene-related mouse DNA sequence SeqID1055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG99925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG99925 standard; DNA; 244
                                                         WPI; 2004-011769/01
                                                                                                                                                                                                                                                                                                                                                                                                                            de an
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(QLJJ/)
(CHEN/)
                                                                                                                                                              (KANS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for diagnosing and/or treating disease activity the S2 serine protease, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated S2 serine protease nucleic acids and polypeptides, useful for diagnosing and/or treating diseases with aberrant expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Darrow AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-2002; 2002US-00189099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ANDR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1011 ATGCACCTGGCCCTTCCCGCC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 ATGCACCTGGCCCTTCCCGCC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 100.
21; Conservative
                                                                                                                                                              KANSAI TECHNOLOGY LICENSING ORG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DARROW A L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHEN C.
                                                                                                          Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isease; proximal tubule; nephrotropic; chronic renal failure;
renopathy; mouse; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ي</u>
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,J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                       Imai E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                          Okubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andrade-Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 8
ABL9980/c
ID ABL998
XX ABL998
XX ABL998
XX O3-OCT
XX Human;
KW Human;
KW SPTM-r
KW Severe
KW Immune
KW Immune
KW Immune
XX Human;
KW Neuros
KW Homo s
XX Homo s
XX O3-OCT
XX

XX O6-SEP
PR 05-SEP
PR 06-SEP
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Best Local Similarity
                                                                        06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
                                                                                                                                                                        06-SEP-2000;
06-SEP-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                              05-SEP-2000;
05-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ss; gene; secretory protein; secretory polynucleotides; SPTM; SPTM-related disease; somatic gene therapy; germline gene therapy; severe combined immunodeficiency; intracellular parasite protection; fungal parasite; protezzoan parasite; cell proliferative disorder; cancer; immune disorder; AIDS; neurological disorder; Parkinson's disease; motor neuron disorder; demyelinating disease; multiple sclerosis;
                                                                                                                                                                                                                                   06-SEP-2000;
                                                                                                                                                                                                                                                                           05-SEP-2000;
                                                                                                                                                                                                                                                                                             05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-2001; 2001WO-US027297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meningitis; abscess; prion diseases; cerebral paley; neuroskeletal disorder; peripheral nervous system disorder; dermatomyositis; polymyositis; myopathy; myasthenia gravis; mental disorder; Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel kidney disease-associated genes expressed in proximal tubules. The invention may be useful for the development of compounds with a nephrotropic activity. The genes are applicable in the diagnosis of, in drug development and in devising appropriate strategy in the treatment of (for example) chronic renal failure and diabetic
                                                                                                                                                                                                                                                       05-SEP-2000;
                                                                                                                                                                                                                                                                                                                05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200220756-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL99890 standard; cDNA; 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL99890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 244 BP; 55 A; 67 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     renopathy. The present sequence is that of a mouse DNA sequence which is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis
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                2000US-0230514P
2000US-0230515P
2000US-0230518P
2000US-0230518P
2000US-0230519P
2000US-0230596P
2000US-0230596P
2000US-0230597P
2000US-0230597P
2000US-0230664P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of, in drug development and in devising appropriate strategy of e.g. chronic renal failure and diabetic renopathy.
                                                                                                                                                                                                                                 2000US-0230583P.
2000US-0230505P.
                                                                                                                                                                                                                                                                                             2000US-0229751P
                                                                                                                                                                                                                                                                                                                2000US-0229750P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO 1055; 770pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (sptm) 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
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18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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RESULT 9
ADQ87121/
ID ADQ8
XX ADQ8
XX ADQ8
XX ADQ8
XX Huma
XX Huma
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Best Local :
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06-SEP-2000;
06-SEP-2000;
07-SEP-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM DNA sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in providing protection against intracellular parasites (e.g. fungal parasites and protection against intracellular parasites (e.g. fungal parasites and proteozoan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer, immune disorders (e.g. AIDS), neurological disorders (e.g. Parkinson's disease), motor neuron disorders demyelinating diseases (e.g. multiple
                                                                                                                                                                                  Human tumour-associated antigenic target (TAT) cDNA sequence #3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sclerosis), meningitis, abscesses, prion diseases, cerebral palsy, neuroskeletal disorders, peripheral nervous system disorders, derimprositis, myopathy, myasthenia gravis, and mental disorders (e.g. Tourette's syndrome). cDNA sequences ABL99746 - ABL99929
                                                                                                                                human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                     07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide sequences encoding human secretory proteins useful gene therapy of e.g. genetic deficiency disorders, cancers, and dicaused by intracellular parasites.
                                                                    WO2004060270-A2
                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                     ADQ87121;
                                                                                                                                                                                                                                                                                   ADQ87121 standard; cDNA; 3157 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1795 BP; 350 A; 585 C; 502 G; 358 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 336-337; 585pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marwaha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Momiyama
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07-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                          1006 CACTGATGCACCTGGCCCTTC 1026
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                                                                                                                                                                                                                                                                                                                                                                     CACTGATGCACCTGGCCCTTC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lincoln SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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2000US-0230897P.
2000US-0230951P.
2000US-0231163P.
2000US-0231163P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                incoln SE, Altus CM, Dufour GE, Chalup MS, U JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Bradley DL, Rohatgi SD, Harris B, Roseberr Peralta CH, David MH, Panzer SR, Flores V, Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0230988P
2000US-0230989P
2000US-0230990P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises the amino acid and coding sequences of human TM) proteins. The SPTM DNA and amino acid sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secretory polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1795;
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B, Roseberry AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CC sequence identity to (a) -(c); (c) a sequence that hybridises to (a) -(c); (c) an expression vector comprising the above (c). Also described: (1) an expression vector comprising the above mucleic acid; (2) a host cell comprising the above expression vector; (3) CC a process for producing a polypeptide; (4) an isolated polypeptide (c) approaches for producing a polypeptide; (4) an isolated polypeptide (c) an isolated polypeptide; (6) an amino acid sequence encoded by any of the above nucleotide sequences; or (c) a sequence (c) length coding region of the above nucleotide sequences; or (c) a sequence (c) an isolated antibody (b) an amino acid sequence encoded by the full-(c) an isolated antibody (b) an isolated oligopeptide by the full-(c) composition of matter comprising the above polypeptide; (7) a process (6) CC an isolated antibody; (8) an isolated oligopeptide; (7) a process (6) CC in above polypeptide; (9) a tumour-associated antigenic target (TAY) (c) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide; (10) a composition of matter comprising to the above polypeptide; (10) a composition of matter contained within the container; (12) methods of cinhibiting the growth of a cell that expresses the above protein, where CC inhibiting the growth of a cell that expresses the above protein, where CC presence of a protein in a sample suspected of containing the protein container; (12) amethod of determining the protein and (17) amethod of determining the protein; (14) a method of determining the protein; (14) a method of determining the protein and contained with increased expression or activity of the above composition and methods and an antibody, oligopeptide or composition and methods of an antibody, oligopeptide or composition and methods of containing the protein described above. CC protein, and (17) amethod of determining the protein described above. The following the composition of activities, and can be used for preparing 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3997; 5504pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-534300/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences (a); (c) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       target (TAT) nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated tumour-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-OCT-2002; 2002US-0418988P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAT) nucleic acid comprising: (a) any of 4622 nucleotide is (see SEQ ID NO:1 to 4622); (b) the full-length coding the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (b) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) a sequence that has 8 in the complement of (a) or (b); (d) and (d) or (b); (d) and (d) or (b) or (
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ABZ36074/c
ID ABZ360
XX
AC ABZ360
XX
                                                 RESULT 10
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Best Local S
Matches 21
                              ABZ36074 standard; cDNA; 3983
                                                                                           1006 CACTGATGCACCTGGCCCTTC 1026
                                                                              541
                                                                                                                               Similarity
                                                                                                                      Conservative
                                                                                                                    2.0%; Score 21;
100.0%; Pred. No.
cive 0; Mismatc
                              먪
                                                                              521
                                                                                                                      Mismatches
                                                                                                                             16;
                                                                                                                                        12;
                                                                                                                     0,
                                                                                                                                       Length 3157;
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밁 S

Sequence 3157 BP;

636

A; 1026 C; 812 G;

683

T; 0 U; 0 Other

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Gaps

0

ABZ36074;

10-FEB-2003

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polynucleotide

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Matches
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Daughtery S
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29-MAR-2001;
16-MAY-2001;
17-MAY-2001;
17-MAY-2001;
19-JUN-2001;
20-JUN-2001;
                                                                                                                                                                  naturally occurring polynucleotide sequence at least 90 % identical to the polynucleotide sequence, a polynucleotide complementary to them or an RNA equivalent of them. The polypeptide or polynucleotide are useful for treating, preventing or diagnosing a disease or condition associated with the expression of functional SPTM. These are particularly useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease) neurological disorders (e.g. cpilepsy, Huntington's disease, dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease, multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety, schizophrenia or amnesia), or cell proliferative disorders (e.g. schizophrenia or amnesia), or cell proliferative diseaser (e.g.
                                                                                         psoriasis, polycythemia vera, or cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain, breast, cervix or prostate). Note: The sequence data for this patent did not form part of the printed specfication, but was obtained in electroni format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                         New human secretory proteins and polynucleotides, useful for diagnosing treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus; secretory polynucleotide; secretory protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple sclerosis; Parkinson's disease; cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; cell proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2002; 2002WO-US009921
                                                             Sequence 3983 BP;
                                                                                                                                                                                                                                                                                                                                               comprising any of 567
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
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                 Local
   Similarity 21; Conserv
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Y SC, David MH,
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; 2001US-0280068P.
; 2001US-0291280P.
; 2001US-0291829P.
; 2001US-0291849P.
; 2001US-029428P.
; 2001US-0299776P.
; 2001US-0300001P.
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disorder; inflammatory disorder; AIDS; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                             ID NO
                                                                                                                                                                                                                                                                                                                                                              relates to a secretory polynucleotide (designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENOMICS INC.
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                   Pred. No.
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A, Chen
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Nguyen DA, Kleefe
N, Chen AJ, Panzeı
In RY, Urashka ME;
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O, Yap PE, A
DA, Kleefeld
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                                                                         The present invention describes an isolated polynucleotide (I): (a) CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b) CC which encodes a polypeptide with biological activity, where the CC polynucleotide hybridises to (I) under stringent hybridisation conditions or has greater than 99% sequence identity with (I). (I) has respiratory, CC cytostatic, antiarthritic, antiinflammatory, gastrointestinal, (CC antibacterial, immunosuppressive, antidiabetic and antirheumatic contributes, and can be used in gene therapy. (I) can be used for CC generating polynucleotides encoding chimeric or fusion proteins and CC express recombinant protein for analysis, characterisation or therapeutic use; as markers for tissues in which the corresponding protein is CC use; as markers or tags to identify chromosomes or to map related gene chromosome markers or tags to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to CC identify potential genetic disorders; as probes to hybridiae and discover genes, related DNA sequences; as a source of information to derive PCR CC genes, related DNA sequences; as a probe to subtract-out known constraints and making oligomers for attachment to a gene chip or other support, including for examination of expression patterns; to raise anti-generation artifical patterns; and as an antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
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protein antibodies using DNA immunisation techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. The polynucleotides and polypeptides can also be used as nutritional source.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotides and polypeptides, useful for treating, e.g. cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-2001; 2001US-0306971P
28-MAR-2002; 2002US-00112944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastrointestinal; antibacterial; immunosuppressive; antidiabetic; antirheumatic; gene therapy; molecular weight marker; chromosome marker chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiratory;
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D, Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type I or graft versus host disease. The present sequence represents a novel human polynucleotide sequence from the present invention. N.B. The sequences for this patent were obtained from the USPTO web site from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a mammal that will respond therapeutically to a method of treating cancer comprises comparing the level of a biomarker in a mammal before and after exposure to an epidermal growth factor receptor (EFGR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; gene; cytostatic; epidermal growth factor
identification; therapeutic response; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tatic; epidermal growth factor receptor modulator; therapeutic response; cancer; EGFR; biomarker.
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Pred. No.
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The invention relates to a method of identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidermal growth factor receptor (EGFR) modulator by comparing the level of a biomarker in a mammal before and after exposure to an EGFR modulator. The method comprises: (a) measuring, in the mammal, the level of at least one biomarker identified in the specification, (b) exposing the mammal to the EGFR modulator; and (c) measuring in the mammal the level of the biomarker, where a difference in the level in step (c) compared to step (a) indicates that the mammal will respond

therapeutically

to the

method

of treating cancer.

Query Match

Sequence

189013 BP;

53603 A;

38975 Score

Ç 21;

39348 BB

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57087 T;

0 U,

0 Other;

8;

Disclosure; SEQ ID NO 26; 520pp; English.

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                                                             potentially harmful treatment of those subjects who do not respond to the treatment with substances (nonresponders), as well as the development of drug resistances due to suboptimal drug dosing can be avoided. ACF62200 to ACF62751 and ABM34912 to ABM35013 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                     treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a cytochrome p450, subfamily IIIA (nifediplne oxidase), polypeptide 5 (CYP3A5) polymucleotide (II). (I) and (II) have cytostatic activity. The therapeutic applications of (I) is improved, since it is possible to individually treat a subject with an appropriate dosage and/or an appropriate derivative of (I). Therefore, undestrable, harmful or toxic effects are efficiently avoided. Unnecessary and
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes the use of irinotecan (I) or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New use of irinotecan for preparation of compositions for treating in subject having genome with variant allele comprising cytochrome subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma; cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide cytostatic; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 669; 86pp;
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2002EP-00011710.
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                                                                                                                                                   The present invention describes a method for the use of irinotecan (I) of its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance protein I (MRPI) polynucleotide (II). (I) has cytostatic activity. (I) or its derivative can be used for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject, where the subject is a human preferably African or Asian) or a mouse. The present sequence represent
                                                                                                                                                                                                                                                                                                                                                        Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         irinotecan; colorectal cancer; cervical cancer; gastric cancer;
lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
variant allele; multidrug resistance protein 1; MRP1; cytostatic;
                                                                                                             Sequence 189013
                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 669; 100pp; English.
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24-MAY-2002; 2002EP-00011710.
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                                                                                                                                          sequence which is
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              114 TGTCTGAGGCCACACAGCTAG
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TGTCTGAGGCCACACAGCTAG 4142
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100.0%; Pr
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tive 0; Mismatches
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RESULT 15 ADB87945/c ID ADB87945 standard; DNA; 189013

Search completed: June Job time : 686 secs

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                                                                                                                                                                    The invention relates to the novel use of irinotecan to treat a patient suffering from cancer. This involves determining if the patient has one or more variant alleles of the UGTIA1 gene, and if the patient has one or decreased amount in comparison to the amount that is administered without regard to the patient's alleles in the UGTIA1 gene. The invention has cyrostatic activity. A composition of the invention acts as a topoisomerase I inhibitor. The method is useful for treating a patient, an animal e.g. mouse or a human, preferably African or Asian, suffering from cancer such as colorectal, cervical, gastric cancer, lung, ovarian, pancreatic cancer, or malignant glioms. The present sequence is udes in
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Use of irinotecan to treat cancer patient by determining if patient has variant alleles of UGT1A1 gene, administering increased/decreased amounts of irinotecan based on increased/decreased levels of UGT1A1 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rinotecam; cancer; UGTIA1; cytostatic; topoisomerase I inhibitor; colorectal cancer; cervical cancer; gastric cancer; lung cancer; ovarian cancer; pancreatic cancer; malignant glioma; uridine diphosphate glycosyltransferasel member A1; gene; ds.
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24-MAY-2002; 2002EP-00011710.
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                                                                                                                                                          exemplification of the invention.
4162 TGTCTGAGGCCACACAGCTAG
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                                                                             Similarity
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                             TGTCTGAGGCCACACAGCTAG 134
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Result
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-6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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equence 4536, A equence 10837, equence 622, Ap	Sequence 740, App Sequence 4528, Ap Sequence 53528, A Sequence 925, App Sequence 836, App	equence 502, equence 502, equence 129, equence 1210 equence 1210		equence 54, equence 695, equence 340, equence 391, equence 74,	equence 105 Sequence 69 Sequence 10 Sequence 14 Sequence 14 Sequence 13 Sequence 13	Sequence 196, App Sequence 669, App Sequence 7, Appli Sequence 7, Appli Sequence 195771, Sequence 195771, Sequence 1058, Ap

## ALIGNMENTS

RESULT 1 US-10-189-099A-1

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                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1038; Conservative 0
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3006
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APPLICANT: Darrow, Andrew L
APPLICANT: Qi, Jian-shen
APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon,
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                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/189,099A
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Human PRSS-11 like
1 CAGGGACTCGAAGTTTGCAGTCCTCCACACTCAGTTCCCACAGATGTGGTAGGAGGGCAT
                                       CAGGGACTCGAAGTTTGCAGTCCTCCACACTCAGTTCCCACAGATGTGGTAGGAGGGCAT
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Pred. No. 0;
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; GENERAL INFORMATION:
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; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Cailin
; APPLICANT: Chen, Cailin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 ser
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/617,443B
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-10-102-806-82/c
Sequence 82, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
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                                                                                                                                                                                                             RESULT 4
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US-09-925-298-82/c
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 82, Application US/09925298 Publication No. US20020039764A1
                                                                                                                                                                                                                                                                                                                                                                                Query Match
 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PALO3PIC1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (1363)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (1378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1379
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
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100.0%; Pred. No.
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                                                                                                                                                                    Sequence 5, Application US/10189099A Publication No. US20040005659A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 82
                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity 100.0%;
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Best Local :
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Human PRSS-11 like S2 serine
FILE REFERENCE: ORT-1644
CURRENT APPLICATION NUMBER: US/10/189,099A
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets
FILE REFERENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/417,375
CURRENT FILING DATE: 2003-04-15
                                                                                                           APPLICANT: Darrow, Andrew L
APPLICANT: Qi, Jian-shen
APPLICANT: Chen, Cailin
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LOCATION: (1365)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (1378)
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NAME/KEY: misc_feature
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nes 22; Conserv
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Pred. No.
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Pred. No. 0.54;
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RESULT 8
US-10-112-944-196/c
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APPLICANT: Qi, Jian-shen
APPLICANT: Qi, Jian-shen
APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Human PRSS-11 like S2 ser
FILE REFERENCE: ORT-1644
CURRENT APPLICATION NUMBER: US/10/617,443B
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: primer US-10-189-099A-5
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Best Local Similarity
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SEQ ID NO 5
LENGTH: 34
TYPE: DNA
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APPLICANT:
APPLICANT:
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               CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
                                              APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids
TITLE OF INVENTION: Secreted Polypeptides
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 PRIOR APPLICATION NUMBER:
                                                                                                                                                                    APPLICANT:
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SEQ ID NO 5
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ORGANISM: Artificial Sequence
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nes 21; Conserv
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                                                                                                                                             Wehrman, Tom
Ghosh, Malabika
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Wang, Jian-Rui
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Weng, Gezhi
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o. US20040048249A1
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US 09/488,725
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-484-577-669
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Best Local S
Matches 21
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SOFTWARE: pt_FL_genes Version 5.0
SEQ ID NO 196
                                                                                         Matches
                                                                                                                                  Query Match
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (985)..(3036)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(4030)
OTHER INFORMATION: n = a,t,c or
                                                                                                                                                                                                                                                                                                                        APPLICANT: EPIDAURÓS Biotechnologie Aktiengesellschaft
TITLE OF INVENTION: Means and methods for improved treatment of cancer based on UGT1A1
FILE REFERENCE: F2285PCT-1
CURRENT APPLICATION NUMBER: US/10/484,577
CURRENT FILING DATE: 2004-01-22
PRIOR APPLICATION NUMBER: PCT/EP 02/08220
PRIOR FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: EP 01 11 7608.8
PRIOR APPLICATION NUMBER: EP 01 11 7608.8
PRIOR PILING DATE: 2001-07-23
PRIOR PILING DATE: 2001-07-23
PRIOR PILING DATE: 2001-07-23
PRIOR PILING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-23
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 683
SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
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PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR APPLICATION NUMBER: US 09/552,929
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APPLICATION NUMBER: US 09/515,126
FILING DATE: 2000-02-28
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APPLICATION NUMBER: US 09/496,914
                                         114 TGTCTGAGGCCACACAGCTAG 134
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TGTCTGAGGCCACACAGCTAG 4142
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100.0%; Pred. No.
tive 0; Mismatc
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00.0%; Pred. No.
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RESULT 12

US-10-027-632-195771/c

; Sequence 195771, Application US/10027632

; Publication No. US20020198371A1
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US-10-617-443B-7
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               GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
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Best Local Similarity
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SEQ ID NO 7
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TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
FILB REFERENCE: ORT-1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Darrow, Andrew L
APPLICANT: Qi, Jian-shen
APPLICANT: Chen, Cailin
APPLICANT: Andrade-Gordon,
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CURRENT APPLICATION NUMBER: US/10/189,099A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE:
URRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Internal Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Internal Sequence: primer
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; ORGANISM: Human
US-10-027-632-195771
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US-10-027-632-195771
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SOFTWARE: FastSEQ for
SEQ ID NO 195771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 195771, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                  Matches
                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/146,002
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CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/156,358 FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/167,363
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                                67 TCCCATTTTCAGATGAGGA 86
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TCCCATTTTCAGATGAGGA 445
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                                                                Conservative
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Pred. No.
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7.1;
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RESULT 15

US-09-833-263-1058/c
US-09-833-263-1058/c
Sequence 1058, Application US/09833263
; Patent No. US20020110547Al
; GENERAL INFORMATION:
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
APPLICANT: Meagher, Madeleine J.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
; SOPTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1058
; SEQ ID NO 1058
; SEQ ID NO 1058
; CRGANISM: Homo sapiens
US-09-833-263-1058
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APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121. 471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1058
LENGTH: 15720
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US-09-922-217-1058/c
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; ORGANISM: Homo sapiens
US-09-922-217-1058
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Search completed: June 29, 2005, 21:23:40 Job time: 763 secs
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Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
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                                                                                                                                                                          Query Match 1.9%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 5.: Matches 20; Conservative 0; Mismatches
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APPLICANT:
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Benson, Darin R.
Meagher, Madeleine Joy
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Minimum DB
Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                 Score
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Match Length DB
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10294.006 Million cell updates/sec
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AC137629 Homo sapi
AC002419 Homo sapi
AL002413 Mouse DNA
AC104081 Homo sapi
AL445683 Human DNA
AC005815 Homo sapi
AC010768 Homo sapi
AC010768 Homo sapi
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AC118993 Rattus no
AC110369 Rattus no
AC110369 Rattus no
AC012621 Homo sapi
AC003108 Human Chr
AC031767 Homo sapi
AC031786 Human DNA
AL1356748 Human DNA
AL157934 Human DNA
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AL445986	BX649374	AC106346_1	HS599F21	AL162399	HUAC004097	AF338323	AY504960	AF075576	BC027716	BC040351	BC015726	AK025714	CR456444	CQ730199	BC026545	AX740556	BC083769	AF172275	AC128818	AC094523	AC108561	BX842698	AL845161	AC006288	AC145423
AL445986 Human DNA	BX649374 Sminthops	Continuation (2 of	AL035662 Human DNA	AL162399 Human DNA	AC004097 Human Chr	AF338323 Mus muscu	AY504960 Homo sapi	AF075576 Mus muscu	BC027716 Homo sapi	BC040351 Homo sapi	Homo	AK025714 Homo sapi	CR456444 Homo sapi	CQ730199 Sequence	BC026545 Mus muscu	AX740556 Sequence	BC083769 Rattus no	AF172275 Mus muscu	AC128818 Rattus no	AC094523 Rattus no	AC108561 Rattus no	BX842698 Mus muscu	AL845161 Mouse DNA	AC006288 Homo sapi	AC145423 Homo sapi

## ALIGNMENTS

REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	RESULT 1 AC113611 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM
MO 63108, USA 6 (bases 1 to 60597) Waterston, R. Direct Submission	5 (bases 1 to 60597) Waterston,R.H. Direct Submission Submitted (23-FBB-2003) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,	4 (bases 1 to 60597) 4 (bases 1 to 60597) Waterston,R.H. Direct Submission Submitted (11-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA	sequence published (bases 1 cerston, R rect Submitted ()	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 60597)  Sulston, J.E. and Waterston, R.  Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)  99063792  9847074  2 (bases 1 to 60597)  Task A and Cotton M.	AC113611 60597 bp DNA linear PRI 10-MAR-2003 Homo sapiens BAC clone RP11-421M20 from 4, complete sequence. AC113611 AC113611.3 GI:28475761 HTG. Homo sapiens (human)

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
This sequence is not the entire insert of the clone. This clone
overlapped by AC104650 and AC104825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Data from
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
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                              /rpt_family="AT_rich" 5208. .5410
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3500. .3682
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
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                                                                                                                                                                                                                              rpt_family="(CAGAGA)n"
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780 21328	721 GCTCACGGCAATATCCTAACCTCTCTGAGCCTCCTGCCCAGCCTAGCAGGTCCAGTG	음 중
720 21268	661 GGAACAGACAAGGCCCAGGGGGACTAACCCGAGATCCAGCCCCGGGCTCACTCCCGTGTG	음 성
660 21208	601 AGCTGGAGCCCATGAGGAGAGGGCCAGTTCTCTCCTGTAAGGGTATTGCTGTAGCATGAG	음 성
600 21148	541 GGGGTCTTCCACTACACCCCCGCCTGGACACTGCTGTAGCCCCAGGGCTCGGAGGGACCC	
540 21088	481 CTCTTTTGGCCCAGAGGGGCCACGCTGTGTCCGGGCCTGGGTAGCTCAGAAGGGTCACCT	유 성
480 21028	421 GGCTGGGGTGTGGCCAAGTTAGACACAGATGTAGGGCCCTGTGGACTCAGAAATTGGCAG	
420 20968	361 GCAGCAGGAATCTGAGCCCGGGAAGGGTCCAGGGAAGTTCGTGAACCATCTAGCAAGTCG	유 성
360 20908	301 CCCGTGCCACTGCATGCCTCAGGCCTGTGGTCCTGGCAGGCCACAGGCCCCTACTGCTGACG	음 성
300 20848	241 TGGTGGGAACTGGAGAGAGCCCGGCACAGGCCCGTGCAGGGAACCCCCGAGGGCTGTAGGC	ት
240 20788	181 CCAGTTGCTCATTGCGGGGGCTCGGGAGCCACGAGGCAGGC	음 성
180 20728	121 GGCCACACAGCTAGAAAGCAGCCAGGCCCAGCCGAACCCCTGGTGTGTGCAGCCCCCAGC	음 성
120 20668	61 ATTCAGTCCCATTTTTCAGATGAGGAGTTGAGGCCCAGAGAACGTAAGTAA	음 성
60 20608	1 CAGGGACTCGAAGTTTGCAGTCCTCCACACTCAGTTCCCACAGATGTGGTAGGAGGGCAT	음 성
0,	Query Match 80.3%; Score 834; DB 9; Length 60597; Best Local Similarity 99.6%; Pred. No. 0; Matches 1034; Conservative 0; Mismatches 4; Indels 0; Gaps	
	repeat_region 29988.30078 /rpt_family="MIR" repeat_region 30801.30893	
	repeat_region 2840628597 /rpt_family="MER1_type" repeat_region 2961329783 /rpt_family="NER1_type"	
	epeat_regio	
	/rpt_family="Alu" repeat region 2775528016	

OR NI TI	em T	B &	8 8		Ş		\$ B
100 Rattus norvegicus clone CH230-237HB, WORKING DRAFT SEQUENCE, 2 unordered pieces.  AC11893 AC11893.4 G1:55013258 AC11893.4 G1:55013258 AC11893.4 G1:55013258 AC11893.4 G1:55013258 AC11893.4 G1:55013258 S HTG; HTGS PHASEI, HTGS DRAFT; HTGS FULLTOP. Rattus norvegicus (Norway rat) Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus norvegicus (Norway rat) 1 (bases 1 to 235102) 12 (bases 1 to 235102) 13 (bases) 1 to 235102) 14 (bases) 1 to 235102) 15 Muzny, D. Marie. Metaroa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus norvegicus 1 (bases) 1 to 235102) 15 Muzny, D. Marie. Metaroa; Chordata; Craniata; Vertebrata; Buteleostomi; Rattus norvegicus 1 (bases) 1 to 235102) 16 Muzny, D. Marie. Metaroa; Chordata; Craniata; Vertebrata; Buteleostomi; Rattus 1 (bases) 1 to 235102) 17 Muzny, D. Marie. Metaroa; Chordata; Craniata; Vertebrata; Buteleostomi; Rattus 1 (bases) 1 to 235102) 18 Muzny, D. Marie. Metaroa; Chordata;		1021 CCCTTCCCGCCAGCGCAG 1038	761 IGCCCACTGGGCATAGGCCTCTGGGAGCTGGCAGCATCGTGATCTCACTGATGCACCTGG 21568 21509 TGCCCACTGGGCATAGGCCTCTGGGAGCTGGCAGCATCGTGATCTCACTGATGCACCTGG 21568	AGTGTGGGCTGAGGCTGTGAACTGGGACAGGGGTGTCTCAGGAAGAGCCTCCTTCC 2	901 AGTGTGGGCTGAGCTTGGAACTGGGACAGGGGTCTCAGGAAGAGCCTCCTCCTCC 960		21329 AGGGGGTGAGGAAGCCCAGCACGTGGAAGCCTTTTTAACCATTCTCGGGGTGAGCGAGC

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JOURNAL
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Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23681105.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Submitted (24-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Havlor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C. Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K. valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wujht, R., Wakub, S., Yen, J., Yoon, L., Yoon, V., F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baylor Plaza, Houston,
3 (bases 1 to 235102)
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                                                                                                                                                                                                                                                                                                                                                                                            (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 235102)
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Center clone name: CH230-237H8
Center clone name: CH230-237H8
Center clone name: CH230-237H8
Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 227037 bases at least Q30
Consensus quality: 229537 bases at least Q30
Consensus quality: 231225 bases at least Q20
Estimated insert size: 235071; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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/note="wgs_end_extension
                                                                                                            organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                        9 108168: gap of unknown le
9 235102: contig of 126934
Location/Qualifiers
                                                                     clone="CH230-237H8"
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89157 CATGCCTCAGGCCTGTGGTCCTGGCA 89132
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Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Narkervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Neasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pinues, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartebeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
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complement(3003.
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[69. .110729
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C. Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K. Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, R., Weite, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, R., Weite, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, R., Weite, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiner, R., Weite, R., Smith, D.R., Holt, R.A., Smith, H.O., Weite, R., Weite, R., Smith, D.R., Holt, R.A., Smith, H.O., Weite, R., Weite, R., Smith, D.R., Holt, R.A., Smith, H.O., Weite, R., Weite, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (11-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Niederhausern, A., Weiss, R., Weinstock, G. and Gibbs, R.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This sequence may represent more than one clone. NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 258368)
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249358
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Consensus quality: 236348 bases at least Q40
Consensus quality: 23637 bases at least Q30
Consensus quality: 240713 bases at least Q20
Estimated insert size: 259061; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
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                                                                                                                                                                                                                                                                                                                                                                                                      1. .258368
                               note="wgs_end_extension
lone_end:T7"
                                                                                                                                                                                                /clone="CH230-49K10"
                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102159: contig of 102159 bp in length 102259: gap of unknown length 249257: contig of 146998 bp in length 249357: gap of unknown length 258368: contig of 9011 bp in length.
                                                                                                                                                      1248
                                                                                                                                                                                                                                                    xref="taxon:10116"
                                                                                                                                                                                                                                                                                                   type="genomic
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SOURCE
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KEYWORDS
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AC134075
LOCUS
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davis, C., Davis, C., Davis, C., Dathorne, S.R., David, R., Delaney, K.R., Davis, C., Dary-Carroll, L., Dederich, D.A., Delaney, K.R., Dayado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferragutco, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hemandez, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Martis, C., Harris, K., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratsori, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratsori, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratsori, E., Mawhiney, E., McLeod, M.P., Meadox, M., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mahiney, E., McLeod, M.P., Meadox, M., Muyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwoon, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Oulles, M., Ren, Y., Sudergre, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82091 CATGCCTCAGGCCTGTGGTCCTGGCA 82066
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26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J. Ranton T Bi----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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site:EcoRI
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102260. .104120
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78223. .79518
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rative 0; Mismatches
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Pred. No. 0.0057;
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On Nov 13, 2002 this sequence version replaced gi:23267440.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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Submitted (22-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 264075)
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
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                                                                                             /note="wgg_end_extension
clone_end:T7"
1858.~.15329
/note="clone_boundary
clone_end:T7
end_sequence:BH287375"
258169..258875
/note="clone_boundary
clone_end:Sp6
                                                                                                                                                                                                                           clone="CH230-2H18"
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_xref="taxon:10116"
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    Genome Center

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quality: Phrap Quality >=40 100% of
Estimated Total Number of Errors is
Location/Qualifiers
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DOE Joint Genome Institute.
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259534. .262529
/note="wgs_end_extension
clone_end:Sp6"
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                                                                                                                                                                                                                               /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/mol_type="genomic DNA"
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100.0%; Pred. No. 0.005
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Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 18, 2003 this sequence version replaced gi:18542968.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-FEB-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US 4 (bases 1 to 145023)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 (bases 1 to 145023)

DOE Joint Genome Institute.
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2.3%; Score 24; DB 9; llarity 100.0%; Pred. No. 0.085; Conservative 0; Mismatches
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Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: mdadams@tigr.org. The orientation of the sequence is from SP6 end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Meshington), Genscan (Chris Burge,
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Human Chromosome 16 BAC clone CIT987SK-327O24, complete sequence.
ACOO3108
                                                                                                                                                                                                                                                                                                                                                                                    complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hpi/hpi.html). Genes without peptide homolgy having the EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 164564)
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C.
Human Chromosome 16 BAC clone CIT987SK-327024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loftus,B.J., Kim,U.J., Sneddon,V.P., Kalush,F., Brandon,R., Fuhrmann,J., Mason,T., Crosby,M.L., Barnstead,M., Cronin,L., Deslattes Mays,A., Cao,Y., Xu,R.X., Kang,H.L., Mitchell,S., Bichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D. Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q Genomics 60 (3), 295-308 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission Submitted (05-FEB-1998) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-NOV-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/\chris/GENSCANW.html)searches of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams, M.D. and Loftus, B.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams, M.D. and Loftus, B.J. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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complement (joIn(10088. .10235,11499. .11710,14305. 17457. .17562,23632. .23807,28068. .28253,28320. .2/gene="327024.1"
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                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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Eutheria; Primates;
                                                                                                                                                                                                           lone="327024"
                                                                                                                                                                                                                                                                                                               type="genomic
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                                                                                                                 Homo sapiens 12 BAC RP13-942N8 (BAC Library) complete sequence. AC137767 AC137767.16 GI:32140199
Homo sapiens (human)
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MEMETVYSNSEVRNLNVPAIFPNSFPSHTEHSTAAKLDKIAGILPLDNEDQCKTDGID
LARISSEGHNSFKQCDSSNIGHVENRAFPKTSSATPQETLISDGFFSVNEQQDLFLLAE
VIPDFYVMSLQNLMKKSKEYIEREQSRRSLRGSMNRIVNESHLDKEHDAVEVADCVKE
KGQLTGKHCVGVIPDKPSLNKSNVLLQGASTQASSMSMFVLLAFSVCHILINV
LESNSDFKVIFTFVTENNVIKSLTGSYAKLPSPEBRMSFWHARRRRTSSACHILINN
PINACELSPKGKEQANDLIIQDTDERTNVPEIMFKLFTDLAGVCSSKVYVGKNTSEVK
EDVYLGKSNQVCQSSGNHLENKVTHGLVTVEGQLTSDERGAHIMNSTCAAMPKLHEPY
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47273...47403,48499...48676,49233...49372,49490...49606,
51409...51510,51706...51822,52429...52502,53024...53086,
54567...54626,57808...60015)
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/protein id="AACO5803.1"
/db_xref="G1:2833633"
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FSFEPVPSCRALQVLKPRDRISAIAHRGGSHDAPENTLAAIRQGSPIFSGRSSHFLIR
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DIETTSGGIFVLMHDNTVDRTTDGTRALCDLTFGQIRKLUPAANHRLRNDFDDEKIF
LREAVAECLNHNLTIFFDVKGHAHKATEALKKMYMEFPQLYNNSVVCSFLPEVIYKMR
QTDRDVVITALTHRPMSLSHTGDGKRPXDTFMKHFIFVMMDILLDWSMHNILMVLGGIS
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48499. .48676,49233. .49372,49490. .49606,51409. .51510,
57706. .51822,52429. .52502,53024. .53086,54567. .54626,
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product="KIAA0420"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eutheria;

Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
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                                                        Worley, K.C.
Direct Submission
Submitted (21-JUN-2003) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-APR-2003) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
Baylor Plaza, Houston, TX 77030, USA
(bases 1 to 86027)
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Submitted (03-DEC-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Bavlor Plaza, Houston, TX 77030, USA
On Jun 21, 2003 this sequence version replaced gi:31376404 INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                 of Molecular and Human
Baylor Plaza, Houston,
5 (bases 1 to 86027)
                                                                                                                                                                                                                                                     Submitted (04-JUN-2003) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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of Medicine, One
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                                                                                                                              Department
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. only

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVITUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

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FEATURES
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                                                                  complement (4858
                                                                                                                                                                               complement (2669)
                                                                                                                                                                                                                                                           /rpt_family="AluY"
1483. .1780
                                                                                                                                                                                                                                                                                                                                                                                                 note="overlaps bases 116317. .118312"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                   function="clone overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                           clone="RP13-942N8"
                                                                                                                                                  family="MIRb"
                                                                                                                                                                                                                                             _family="AluSx"
                                                                                                                                                                                                                                                                                                   _family="AluSq"
                                                                                                                                    _family="L1MB5"
family="AluJo"
                                                                               _family="AluSg"
                                                                                                          family="Charlie8"
                                                                                                                                                                                                                     family="AluSx"
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                                                                                                                                                                                                                                                                                                               114 TGTCTGAGGCCACACAGCTAGA 135
                                                                                                                                                                                                                                                                                                                                            22;
Submitted (26-SEP-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                 ALB31755 91841 bp DNA linear PRI Human DNA sequence from clone RP13-279N23 on chromosome
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91841)
                                                                                                                  Homo sapiens
                                                                                                                                                         AL831755.9
                                                                                                                                                                         AL831755
                                             Direct Submission
                                                         darrison, E.
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                             fomo sapiens (human)
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complement(10253. .10437)
/rpt_family="MIR"
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[7482, .7568]
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Submitted (03-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 5, 2000 this sequence version replaced gi:11493283.
During sequence assembly data is compared from overlapping clon where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DNA sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/HGP/Chr1
RP13-279N23 is from the library RPCI-13.2 constructed
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1 constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                Direct
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Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTCTGAGGCCACACAGCTAG 134
                                                                                                                                                                                                           (bases 1 to 97559)
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                                                                                                                                                                Submission
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/clone_lib="RPCI-13.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
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100.0%;
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; Pred. No.
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1 clone RP4-686J16 on
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Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
RP4-686J16 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RP4-686J16 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-686J16 is at 1 in this sequence. true left end of clone RP4-655N15 is at 97460 in this sequence. true right end of clone RP4-781D12 is at 1573 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: PCYPACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.chori.org/bacpac/home.htm
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378. .514
                                                                                                                                                                                                                                                                                                                                                                                                    2051. .2205
/note="MIR repeat: matches 78. .252 of consensus"
2328. .2414
                                                                                                                                                                                                                                                                       complement (2908.
                                                                                                                                                                                                                                                                                                                                                              /note="MLT1H repeat: matches 51.
2477. .2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2014. .2416
/note="match: GSS: Em:AQ706294"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AluSx repeat: matches 1.
complement(1745. .2002)
                                             complement (7909.
                                                                                                                    /note="match:
                                                                                                                                                                                                                                                                                         2676. .2813
note="MLTIF repeat: matches 401.
                                                                                                                                                                                                                                                                                                                              1977. .2555
/note="MLT1H repeat: matches 202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                           note="L1P3 repeat: matches 5725.
                                                                                                                                                                                                       note="L2 repeat: matches 2075.
                                                                                                                                                                                                                                                note="match: STS: Em:G18185"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="match: GSS: Em:AQ474986"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="match: GSS: Em:AQ321132"
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romosome="1"
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                                                                                                                    STS:
                                                                    GSS: Em:AQ707880"
                                                  .8281
                                                                                                                  Em:G15587"
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                                                                                                                                                                                                       .2178 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                  .130 of consensus"
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                                                                                                                                                             .5822 of consensus"
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                                                                             26971.
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/note="MIR repeat: matches 106.
8286. .8342
/note="L2 repeat: matches 2691.
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complement(10541. .11084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat:
complement(16832...
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complement(13076. .13897)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ316052" complement(10633. .10966)
                                                                                          /note="match: GSS: complement(26833. .
                                                                                                                              /note="match: GSS: complement(26720. .
                                                                                                                                                                   /note="match: GSS:
complement(26598.
                                                                                                                                                                                                       complement (26592
                                                                                                                                                                                                                                                                                25186. .25354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="AluSx repeat: matches 5. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 2709.
[4198. .14273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13685. .13725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13492. .13591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="match:
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note="Single clone region. Assembly confirmed by
                                                                       note="match: GSS: Em:AQ837606"
                                                                                                                                                                                                                         'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                               note="L1ME1 repeat: matches 5528. .6159 of consensus" 3288. .23435
                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 20. .184 of
                                                                                                                                                                                                                                                                                                                                                                                                         'note="MIR repeat: matches 16. .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7344. .17892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="match: 7109. .17167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 2584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L2 repeat: matches 2673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="match: GSS: Em:AQ743494"
                                                                                                                                                                                                                                                             note="MIR repeat: matches 77.
                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluJ/FLAM repeat: matches 5. .85 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9553. .19654
note="AluJo/FRAM repeat: matches 203. .304 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="AluSq repeat: matches 37. .311 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="31 copies 2 mer aa 74% conserved"
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12857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat: matches 7758. .7913 of consensus"
                                    repeat: matches 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS: Em:AQ700892"
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                                                                                                                                                                                                       .27148
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.17296)
                                                                                            Em: AQ100816"
.27131)
                                                                                                                              Em: AQ619294"
27017)
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27124)
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                                                                                                                                                                                                                                                             .262 of consensus"
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                                    .180 of consensus"
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RESULT 10
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                            Submitted (05-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 6, 2002 this sequence version replaced gi:17381304. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submission corresponding to the overlapping clone, as we submission analy a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                    AL157934
regions were either double-stranded or sequenced with an chemistry or covered by high quality data (i.e., phred qu
                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   AL157934.17 GI:18077665
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human DNA sequence from
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                                                                                                                                                                                                                                                                          (bases 1 to 106497)
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27133. .27439
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/note="Charlie4 repeat:
38191. .38449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="FLAM_C repeat: matches 1. .118 of consensus"
38174. .38190
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38057. .38173
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17307. .37627
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15737. .36047
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3999. .34281
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19562. .29638
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27236. .27568
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100.0%; Pred. No.
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m clone RP11-449M9 on chromosome
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bme Xq13.1-13.3,
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 113 CTGTCTGAGGCCACACAGCTAG 134
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19854 ACAGGGGTCTCAGGAAGAGCCT 19833
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                                                                                                                                                                                                                                                            Novel therapeutic targets in cancer Patent: WO 2004074320-A 209 02-SEP-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert RP11-449M9 It may be shorter because we sequence esections only once, except for a short overlap. The true left end of clone CTD-2530H13 is at 10449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
RP11-449M9 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw.,
                                                                                                                                                                                                                                           Sagres Discovery, Inc
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CQ869788.1 GI:51999587
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                                                                                                                                                                                                                                                                                                          Morris, D.W., Morris, D.W. and Malandro, M.S
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence. The true right end of clone XX-BWXD718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECTOR: pBACe3.6
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/clone_lib="RPCI-11.2"
10905._.11106
                                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DN
/db_xref="taxon:9606"
                                                                                                                                                                                                                   Location/Qualifiers
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|mol_type="genomic DNA"
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map="q13.1-13.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Charca, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., David, R., David, R., David, R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., David, R., Guevare, M., Gunaratne, P., Garza, N., Gill, R., P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Gaccia, A., Garner, T., Garza, N., Gill, R., Garrie, G., Hartis, K., Hartis, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Harris, C., Hartis, K., Harti, M., Hollows, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Karlsson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Khan, U., King, L., Korsh, J., Koyar, C., Kratovic, J., Kureshi, A., Landry, N., Lala, B., Lewis, L.C., Lewis, L. Li, J., Li, K., Landry, N., Lala, B., Lewis, L.C., Lewis, L. Li, J., Li, X., Lucier, A., Jucier, R., Junia, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Moser, M., Polloken, R., Parton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Scherer, S., Scott, G., Shen, H., Shoshtari, N., Stanley, H., Stone, H., Whoden, R., Wacden, S., Warren, R., Wacden, S., Warren, R.
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                                                                                                                                                                                                   Direct Submission
Submitted (27-NOV-2002) Human Genome Sequencing Center, Depared the Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 125836)
                                                        Submitted (05-ARR-2003) Human Genome Sequencing Center, Depar
of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
On Apr 3, 2003 this sequence version replaced gi:29423847.
                                                                                                                                                                                   Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                       Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Homo sapiens (human)
Homo sapiens
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Homo sapiens clone RP11-525N13,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC137629.16 GI:29501835
Apr 3, 2003 this sequence version replaced gi:29423847
------ Genome Center
Center: Baylor College of Medicine
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Homo sapiens (human)
Homo sapiens
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***, 2 unordered pieces.
                                                                                                                                                   Mazzarella,R.
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AC002419.2 GI:21405639
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100.0%; Pred. No.
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Direct Submission
Unpublished (1997)
2 (bases 1 to 128440)
Brownstein,B.H., States,D.J. and Mazzarella,R.
Direct Submission
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 120440)
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Center project name: HERM
Center clone name: RP11-52SN13
Center clone name: RP11-52SN13

Sequencing vector: Plasmid;
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 125202 bases at least Q40
Consensus quality: 125305 bases at least Q30
Consensus quality: 125395 bases at least Q20
Estimated insert size: 136468; sum-of-contigs estimation
Quality coverage: 20x in Q20 bases; sum-of-contigs estimation
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This is a 'near complete' sequence.
NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by the finished sequence as soon as it is available the accession number will be preserved.

1 125836: contig of 125836 bp in length.
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Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
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(12-AUG-1997) Center for Genetics in Medicine, Box 8232,
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                                                                                                                                                                                                                    States, D.J., Schlessinger, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                   931 ACAGGGGTCTCAGGAAGAGCCT 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Louis, MO 63110, USA on Jun 13, 2002 this sequence version replaced gi:2323250 Current status of this project is available at: 'http://genome.wustl.edu/cgm/seq_projects.html' submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e-mail: states@ibc.wustl.edu.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* to soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine, Box 8232 4566 Scott Avenue, St. Louis, MO 63110, USA
                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                       AL844513 13
Mouse DNA sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    David J. States,
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B50 Lincoln Center Drive,
Foster City, CA 94404 USA
e-mail: ellson@genseq.apldbio.com
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Johnson, C
                                                                   Mus musculus
                                                                                                                      AL844513.8
                                                                                                                                          AL844513
                                                                                                                                                        sequence.
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Applied Biosystems Division of Perlin Elmer Corp.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved
                malia; Eutheria; Rodentia; (bases 1 to 131184)
                                                                                   musculus (house mouse)
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58953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="bWXD40"
                                                                                                                        GI:33438736
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58952: gap of 100 bp
128440: contig of 69488 bp in length.
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00.0%; Pred. No.
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m clone RP23-132A3
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                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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2, complete
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Local Similarity
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The property of the sequence of the seque
                                                                                                                                                                                                                                                                                                                                                                                                                        142118 bp
Homo sapiens BAC clone RP11-559A1
AC104081 AC068259
AC104081.2 GI:17977480
HTG.
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-132A3 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
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Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (Dases 1 to 142118)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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/chromosome="2"
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
NRIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-50B16; the clone sequenced to the right is RP11-554H10, 2000 bp overlap. Actual end of this clone is at base position 79619 of RP11-554H10.
                                                                                                                                                   The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (03-JAN-2002) Genome
University School of Medicine,
MO 63108, USA
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Submitted (22-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                               SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restriction digest.
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                                                                                                                                                                                                                                                                                                                                                                                              sequence, see http://genome.wustl.edu/gsc
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Isak, A. and Meyer, R.
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Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0559A01
Drafting Center: WIBR
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4444 Forest Park Parkway, St.
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Data from AC012671 was used to finish this clone, AC068259.
Polymorphisms have been identified between AC012671 and AC068259.
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